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Datum/Date

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Anmeldung Nr./Application No./Demande n°/Patent Nr./Patent No./Brevet n°

99107430.3-2106/

Anmelder/Applicant/Demandeur/Patentinhaber/Proprietor/Titulaire

Sumitomo Chemical Company, Limited

019

COMMUNICATION

The European Patent Office herewith transmits the partial European search report under Rule 46(1) EPC relating to the above-mentioned European patent application.

Copies of the documents cited in the search report are enclosed.

The applicant's attention is drawn to the following:

The search Division informs the applicant that if the European search report is also to cover inventions other than the invention first mentioned in the claims, a further search fee must be paid for each of these inventions, within ONE MONTH after notification of this communication.

If the application has been filed up to 30 June 1999, the search fee in force before 01 July 1999 (EUR 869,-) or the equivalent applicable on the date of payment is payable.

This applies also to the search fees requested under Rule 46(1) EPC.

See also OJ EPO 06/1999, 405.

Moreover, the Search Division considers that the present European patent application does not comply with the provisions of the European Patent Convention to such an extent that it is not possible to carry out a meaningful search into the state of the art on the basis of some of the claims; reference is made to sheet C, which is attached to the search report.

☒ The abstract was modified by the Search Division and the definitive text is attached to the present communication.

☐ Additional set(s) of copies of the documents cited in the European search report is (are) attached as well.

Note to users of the automatic debiting procedure:

Unless the EPO receives prior instructions to the contrary, the search fee(s) will be debited on the last day of the period for payment. For further details see the Arrangements for the automatic debiting procedure, Supplement to OJ EPO 02/1999.

REGISTERED LETTER





ABSTRACT / ZUSAMMENFASSUNG / ABREGE

99107430.3

The invention disclosed relates to raffinose synthase genes comprising a nucleotide sequence hybridizable with a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO: 1-8, and encoding a protein being capable of binding the D-galactosyl group through an α (1 \rightarrow 6) bond to the hydroxyl group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose.



European Patent
Office

PARTIAL EUROPEAN SEARCH REPORT

under Rule 46, paragraph 1 of the European Patent
Convention

Application Number

EP 99 10 7430

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	JP 10 084973 A (AJINOMOTO CO INC) 7 April 1998 (1998-04-07) * SEQ ID NO:4 and SEQ ID NO:5 * & WO 98 49273 A (AJINOMOTO CO INC) 5 November 1998 (1998-11-05) * abstract *	1,11, 16-23	C12N15/54 C12N9/10 A01H5/00
P,X	EP 0 849 359 A (SUMITOMO CHEMICAL CO) 24 June 1998 (1998-06-24) * the whole document *	1,11-23	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12N A01H
LACK OF UNITY OF INVENTION			
<p>The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:</p> <p>see sheet B</p> <p>The present partial European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims.</p>			
Place of search		Date of completion of the search	Examiner
BERLIN		14 March 2000	Schönwasser, D
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

2

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 99 10 7430

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

14-03-2000

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
JP 10084973 A	07-04-1998	AU 8187498 A	24-11-1998
		WO 9849273 A	05-11-1998
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EP 0849359 A	24-06-1998	BR 9706398 A	05-10-1999
		CA 2218448 A	18-06-1998
		CN 1190129 A	12-08-1998
		JP 11215984 A	10-08-1999
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Claim(s) searched incompletely:
1,11

Reason for the limitation of the search:

Claim 1 (as far as invention 1 is concerned) relates to a raffinose synthase gene which comprises a nucleotide sequence hybridizable with a nucleotide sequence selected from the group consisting of (a) a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO:1 and (b) the nucleotide sequence represented by SEQ ID NO:2. Claim 11 relates to a nucleic acid comprising a partial nucleotide sequence of the raffinose synthase gene as defined inter alia in claim 1. Back-translation of the polypeptide generates a very great number of nucleic acid sequences. It is not possible to search an entire database with this enormous set of sequences. The search thus has been limited to the conventional nucleic acid/nucleic acid, protein/protein and protein/six-frame translated nucleic acid comparisons.



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: partially: 1,11-23; completely: 2,3 and 24

A raffinose synthase gene which comprises a nucleotide sequence hybridizable with a nucleotide sequence selected from a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO:1 and the nucleotide sequence represented by SEQ ID NO:2; a raffinose synthase gene comprising a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO:1 or comprising the nucleotide sequence represented by SEQ ID NO:2; a nucleic acid comprising a partial nucleotide sequence of said gene; methods for detecting and amplifying a nucleic acid containing said gene; a method for obtaining said gene; a nucleic acid containing said gene which is joined to a nucleic acid exhibiting promoter activity in a host cell; a vector comprising said gene; a transformant wherein said gene, or said nucleic acid exhibiting promoter activity, or said vector is introduced into a host cell; a method for producing a raffinose synthase and a raffinose synthase comprising the amino acid sequence represented by SEQ ID NO:1.

2. Claims: partially: 1,10-23; completely: 4,5,25

A raffinose synthase gene which comprises a nucleotide sequence hybridizable with a nucleotide sequence selected from a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO:3 or the nucleotide sequence represented by the nucleotide 236 to 2584 of SEQ ID NO:4; a raffinose synthase gene comprising a nucleotide sequence encoding the amino acid sequence represented by SEQ ID NO:3 or comprising the nucleotide sequence represented by nucleotides 236 to 2584 of SEQ ID NO:2; said gene comprising the nucleotide sequence represented by SEQ ID NO:4; a nucleic acid comprising a partial nucleotide sequence of said gene; methods for detecting and amplifying a nucleic acid containing said gene; a method for obtaining said gene; a nucleic acid containing said gene which is joined to a nucleic acid exhibiting promoter activity in a host cell; a vector comprising said gene; a transformant wherein said gene, or said nucleic acid exhibiting promoter activity, or said vector is introduced into a host cell; a method for producing a raffinose synthase and a raffinose synthase comprising the amino acid sequence represented by SEQ ID NO:3.

3. Claims: partially: 1,10-23; completely: 6,7,26

Invention no. 3 relates to subject-matter as defined above for "invention 2", with the exception, that invention no. 3



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

refers to the amino acid sequence represented by SEQ ID NO:5 (and to the respective nucleotide sequence represented by nucleotides 134 to 2467 of SEQ ID NO:6, or to the complete nucleotide sequence represented by SEQ ID NO:6).

4. Claims: partially: 1,10-23; completely: 8,9,27

Invention no. 4 relates to subject-matter as defined above for "invention 2", with the exception, that invention no. 4 refers to the amino acid sequence represented by SEQ ID NO:7 (and to the respective nucleotide sequence represented by nucleotides 1 to 1719 of SEQ ID NO:8, or to the complete nucleotide sequence represented by SEQ ID NO:8).

EUROPEAN PATENT OFFICE

Patent Abstracts of Japan

PUBLICATION NUMBER : 10084973
PUBLICATION DATE : 07-04-98

APPLICATION DATE : 28-04-97
APPLICATION NUMBER : 09111124

APPLICANT : AJINOMOTO CO INC;

INVENTOR : KIDA TAKAO;

INT.CL. : C12N 15/09 A01H 5/00 C12N 9/00

TITLE : RAFFINOSE SYNTHASE GENE,
PRODUCTION OF RAFFINOSE AND
TRANSFORMED PLANT

Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Thr	Val	His	Pro	Gln
1				5					10					15	
Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val	Asp	Gly	Gly	Cys		
				20					25				30		

cited in the European Search
Report of EP99 107430.3
Your Ref.: 66 1271

I

Pro	Val	Ser	Val	Gly	Cys	Phe	Val	Gly	Phe	Asp	Ala	Ser	Glu	Pro	Asp
1				5					10					15	
Ser	Arg	His													

II

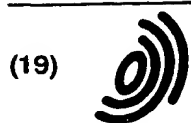
Tyr	Asp	Gln	Asp	Gln	Met	Val	Val	Val	Gln	Val	Pro	Trp	Pro
1				5					10				

III

ABSTRACT : PROBLEM TO BE SOLVED: To obtain a highly active raffinose synthase capable of synthesizing raffinose which has *Bacillus bifidus* proliferative activity and is therefore useful for food materials and organ storage liquids.

SOLUTION: This raffinose synthase is afforded by *Cucumis* plants such as *Cucumis melo* or *Cucumis sativas*, having the following characteristics (1) capable of producing raffinose from sucrose and galactinol; (2) optimum pH is about 6-8, and optimum temperature about at 35-40°C; (3) molecular weight is about 75-95kDa (gel permeation chromatography) or about 90-100kDa (SDS- PAGE, Native PAGE); and (4) containing respective amino acid sequences of formula I to formula III in its amino acid sequence.

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EUROPEAN PATENT APPLICATION

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Remarks:

The applicant has subsequently filed a sequence
listing and declared, that it includes no new matter.

(54) **Raffinose synthetase genes and the use thereof**

(57) Raffinose synthetase genes coding for proteins capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule were isolated from various plants. These raffinose synthetase genes are useful to change the content of raffinose family oligosaccharides in plants.

Description

FIELD OF THE INVENTION

The present invention relates to raffinose synthetase genes and their use.

BACKGROUND OF THE INVENTION

Raffinose family oligosaccharides are derivatives of sucrose, which are represented by α -D-galactopyranosyl-(1 \rightarrow 6) n- α -D-glucopyranosyl-(1 \rightarrow 2)- β -D-fluctofuranoside as the general formula, and they are designated "raffinose" when n = 1, "stachyose" when n = 2, "verbascose" when n = 3, and "ajugose" when n = 4.

The greatest contents of such raffinose family oligosaccharides are found in plants, except for sucrose, and it has been known that they are contained not only in higher plants including gymnosperms such as pinaceous plants (e.g., spruce) and angiosperms such as leguminous plants (e.g., soybean, kidney bean), brassicaceous plants (e.g., rape), chenopodiaceous plants (e.g., sugar beet), malvaceous plants (e.g., cotton), and salicaceous plants (e.g., poplar), but also in green algae, chlorella. Thus, they occur widely in the plant kingdom similarly to sucrose.

Raffinose family oligosaccharides play a role as reserve sugars in the storage organs or seeds of many plants or as translocating sugars in the phenomenon of sugar transportation between the tissues of some plants.

Furthermore, it has been known that raffinose family oligosaccharides have an effect of giving good conditions of enterobacterial flora, if present at a suitable amount in food. Therefore, raffinose family oligosaccharides have already been used as a functional food material for addition to some kinds of food and utilized in the field of specified healthful food.

Raffinose family oligosaccharides having such a role and utility are produced by the raffinose oligosaccharide synthesis system beginning with sucrose in many plants. This biosynthesis system usually involves a reaction for the sequential addition of galactosyl groups from galactotinol through an α (1 \rightarrow 6) bond to a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.

In the first step of this biosynthesis system, raffinose synthetase is an enzyme concerned in the reaction of raffinose production by combining a D-galactosyl group from galactotinol through an α (1 \rightarrow 6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. It has been suggested that this enzyme constitutes a rate limiting step in the above synthesis system, and it has been revealed that this enzyme is quite important in the control of biosynthesis of raffinose family oligosaccharides.

The control of expression level or activity of raffinose synthetase in plants makes it possible to change the contents of raffinose family oligosaccharides in these plants. However, raffinose synthetase, although the presence of this enzyme itself was already confirmed in many plants by the measurement of its activity with a biochemical technique, has not yet been successfully isolated and purified as a homogeneous protein. In addition, the amino acid sequence of this enzyme is still unknown, and no report has been made on an attempt at beginning to isolate a gene coding for this enzyme.

SUMMARY OF THE INVENTION

Under these circumstances, the present inventors have intensively studied and finally succeeded in isolating a raffinose synthetase and a gene coding for this enzyme from broad bean, thereby completing the present invention.

Thus, the present invention provides the following:

- 1) A raffinose synthetase gene isolated from a plant and having a nucleotide sequence coding for an amino acid sequence of a protein capable of producing raffinose by combining a D-galactosyl group through an α (1 \rightarrow 6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.
- 2) The raffinose synthetase gene according to item 1, wherein the plant is a dicotyledon.
- 3) The raffinose synthetase gene according to item 2, wherein the dicotyledon is a leguminous plant.
- 4) The raffinose synthetase gene according to item 3, wherein the leguminous plant is broad bean.
- 5) A raffinose synthetase gene having a nucleotide sequence coding for protein (a) or (b) as defined below:

(a) protein having the amino acid sequence of SEQ ID NO:1;

(b) protein having an amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:1, and capable of producing raffinose by combining a D-galactosyl group through an α (1 \rightarrow 6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.

- 6) A raffinose synthetase gene having the nucleotide sequence of SEQ ID NO:2.
- 7) The raffinose synthetase gene according to item 3, wherein the leguminous plant is soybean.
- 8) A raffinose synthetase gene having a nucleotide sequence coding for protein (a) or (b) as defined below:
 - (a) protein having the amino acid sequence of SEQ ID NO:3;
 - (b) protein having an amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:3, and capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.
- 9) A raffinose synthetase gene having the nucleotide sequence of SEQ ID NO:4.
- 10) The raffinose synthetase gene according to item 2, wherein the dicotyledon is a lamniaceous plant.
- 11) The raffinose synthetase gene according to item 10, wherein the lamniaceous plant is Japanese artichoke.
- 12) A raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of SEQ ID NO:5.
- 13) A raffinose synthetase gene having the nucleotide sequence of SEQ ID NO:6.
- 14) The raffinose synthetase gene according to item 1, wherein the plant is a monocotyledon.
- 15) The raffinose synthetase gene according to item 14, wherein the mono-cotyledon is a gramineous plant.
- 16) The raffinose synthetase gene according to item 15, wherein the gramineous plant is corn.
- 17) A raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of SEQ ID NO:7.
- 18) A raffinose synthetase gene having the nucleotide sequence of SEQ ID NO:8.
- 19) A raffinose synthetase protein having amino acid sequence (a) or (b) as defined below:
 - (a) amino acid sequence of SEQ ID NO:1 or SEQ ID NO:3;
 - (b) amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:3;
the protein being capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.
- 20) A raffinose synthetase protein having the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:3.
- 21) A gene fragment having a partial nucleotide sequence of the raffinose synthetase gene of item 1, 2, 3, 4, 7, 10, 11, 14, 15 or 16.
- 22) A gene fragment having a partial nucleotide sequence of the raffinose synthetase gene of item 5, 6, 8, 9, 12, 13, 17 or 18.
- 23) The gene fragment according to item 21 or 22, wherein the number of nucleotides is in the range of from 15 to 50.
- 24) A method for the detection of a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof, which comprises hybridizing a probe of the labeled gene fragment of item 21, 22 or 23 to an organism-derived genomic DNA or cDNA fragment; and detecting the DNA fragment bound specifically to the probe.
- 25) A method for the detection of a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof, which comprises hybridizing a probe of the labeled gene fragment of item 21, 22 or 23 to a plant-derived genomic DNA or cDNA fragment; and detecting the DNA fragment bound specifically to the probe.
- 26) A method for the amplification of a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof, which comprises annealing a primer having a nucleotide sequence of the gene fragment of item 21, 22 or 23 to organism-derived genomic DNA or cDNA; and amplifying the resulting DNA fragment by polymerase chain reaction.
- 27) A method for the amplification of a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof, which comprises annealing a primer having a nucleotide sequence of the gene fragment of item 21, 22 or 23 to plant-derived genomic DNA or cDNA; and amplifying the resulting DNA fragment by polymerase chain reaction.
- 28) A method for obtaining a raffinose synthetase gene, comprising the steps of identifying a DNA fragment containing a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof by the method of item 24, 25, 26 or 27; and isolating and purifying the DNA fragment identified.
- 29) A raffinose synthetase gene obtained by identifying a DNA fragment containing a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof by the method of item 24, 25, 26 or 27; and isolating

and purifying the DNA fragment identified.

30) A chimera gene comprising the raffinose synthetase gene of item 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 29, and a promoter linked thereto.

31) A transformant obtained by introducing the chimera gene of item 30 into a host organism.

32) A plasmid comprising the raffinose synthetase gene of item 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29 or 30.

33) A host organism transformed with the plasmid of item 32, or a cell thereof.

34) A microorganism transformed with the plasmid of item 32.

35) A plant transformed with the plasmid of item 32, or a cell thereof.

36) A method for metabolic modification, which comprises introducing the raffinose synthetase gene of item 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 29 or 30 into a host organism or a cell thereof, so that the content of raffinose family oligosaccharides in the host organism or the cell thereof is changed.

37) A method for the production of a raffinose synthetase protein, which comprises isolating and purifying a raffinose synthetase protein from a culture obtained by cultivating the microorganism of item 34.

38) An anti-raffinose synthetase antibody capable of binding to the raffinose synthetase protein of item 19 or 20.

39) A method for the detection of a raffinose synthetase protein, which comprises treating a test protein with the anti-raffinose synthetase antibody of item 38; and detecting the raffinose synthetase protein by antigen-antibody reaction between the antibody and the raffinose synthetase protein.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the construction of plasmids used for the expression of a raffinose synthetase gene in *Escherichia coli*. pBluescriptKS-RS is a plasmid containing the raffinose synthetase gene cloned therein. RS represents the raffinose synthetase gene, and the nucleotide sequences shown in the upper portion of this figure are those of both terminal portions of the raffinose synthetase gene. A partial sequence represented by small letters is a nucleotide sequence derived from the vector pBluescriptII KS-. Two boxed nucleotide sequences are the initiation codon (ATG) and termination codon (TGATAA) of the raffinose synthetase gene, respectively. The recognition sites for several restriction endonucleases are shown above the nucleotide sequences. pGEX-RS and pTrc-RS are plasmids used for the expression of the raffinose synthetase gene in *E. coli*. Ptac, Ptrc, GST, lacI^q, and rrnB represent tac promoter, trc promoter, glutathione-S-transferase gene, lactose repressor gene, and termination signal for the transcription of ribosomal RNA, respectively.

Figure 2 shows the construction of expression vectors used for the expression in plants of chimera genes each having a raffinose synthetase gene and a promoter linked thereto. The restriction endonuclease map of the raffinose synthetase gene cloned in the plasmid pBluescriptKS-RS is shown in the lower portion of this figure. pBI221RS and pBI221(-)RS indicate the restriction endonuclease maps of expression vectors used for the transformation of soybean. 35S and NOS represent 35S promoter derived from cauliflower mosaic virus and nopaline synthetase gene terminator, respectively.

Figure 3 shows the construction of expression vectors used for the expression in plants of chimera genes each having a raffinose synthetase gene and a promoter linked thereto. The restriction endonuclease map of the raffinose synthetase gene cloned in the plasmid pBluescriptKS-RS is shown in the upper portion of this figure. pBI121RS and pBI121(-)RS indicate the restriction endonuclease maps of binary vectors used for the transformation of mustard. For the binary vector, only a region between the right border and the left border is shown. 35S, NOS and NPT represent 35S promoter derived from cauliflower mosaic virus, nopaline synthetase gene terminator and kanamycin resistance gene, respectively.

DETAILED DESCRIPTION OF THE INVENTION

The gene engineering methods described below can be carried out according to ordinary methods, for example, as described in "Molecular Cloning: A Laboratory Manual 2nd edition" (1989), Cold Spring Harbor Laboratory Press, ISBN 0-87969-309-6; "Current Protocols In Molecular Biology" (1987), John Wiley & Sons, Inc. ISBN 0-471-50338-X; and "Current Protocols In Protein Science" (1995), John Wiley & Sons, Inc. ISBN 0-471-11184-8.

The term "raffinose synthetase gene" as used herein refers to a gene having a nucleotide sequence coding for the amino acid sequence of a protein capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule (hereinafter referred to simply as the present gene), and such a gene can be prepared, for example, from plants.

More specifically, the present gene can be prepared from dicotyledons such as leguminous plants (e.g., broad bean, soybean) and lamiaaceous plants (e.g., Japanese artichoke) or from monocotyledons such as gramineous plants (e.g., corn). Specific examples of the present gene are a "raffinose synthetase gene having a nucleotide sequence cod-

ing for a protein having the amino acid sequence of SEQ ID NO:1"; a "raffinose synthetase gene having a nucleotide sequence coding for a protein having an amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:1, and capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule"; a "raffinose synthetase gene having a nucleotide sequence coding for a protein having the amino acid sequence of SEQ ID NO:3"; a "raffinose synthetase gene having a nucleotide sequence coding for a protein having an amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:3, and capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule"; a "raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of SEQ ID NO:5"; and a "raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of SEQ ID NO:7."

In a further embodiment, the invention relates to nucleic acid molecules of at least 15 nucleotides in length hybridizing specifically with a nucleic acid molecule as described above or with a complementary strand thereof. Specific hybridization occurs preferably under stringent conditions and implies no or very little cross-hybridization with nucleotide sequences encoding no or substantially different (oligo)peptides. Such nucleic acid molecules may be used as probes and/or for the control of gene expression. Nucleic acid probe technology is well known to those skilled in the art who will readily appreciate that such probes may vary in length. Preferred are nucleic acid probes of 17 to 50, particularly preferred 21 to 50 nucleotides in length. Of course, it may also be appropriate to use nucleic acids of up to 100 and more nucleotides in length. The nucleic acid probes of the invention are useful for various applications. On the one hand, they may be used as PCR primers for amplification of regulatory sequences according to the invention. Another application is the use as a hybridization probe to identify nucleic acid molecules hybridizing with a nucleic acid molecule of the invention by homology screening of genomic DNA libraries. Nucleic acid molecules according to this preferred embodiment of the invention which are complementary to a nucleic acid molecule as described above may also be used for repression of expression of a gene comprising such regulatory sequences, for example due to an antisense or triple helix effect or for the construction of appropriate ribozymes (see, e.g., EP-B1 0 291 533, EP-A1 0 321 201, EP-A2 0 360 257) which specifically cleave the (pre)-mRNA of a gene comprising a nucleic acid molecule of the invention. Selection of appropriate target sites and corresponding ribozymes can be done as described for example in Steinecke, Ribozymes, Methods in Cell Biology 50, Galbraith et al. eds Academic Press, Inc. (1995), 449-460. Furthermore, the person skilled in the art is well aware that it is also possible to label such a nucleic acid probe with an appropriate marker for specific applications, such as for the detection of the presence of a nucleic acid molecule of the invention in a sample derived from an organism.

The above described nucleic acid molecules may either be DNA or RNA or a hybrid thereof. Furthermore, said nucleic acid molecule may contain, for example, thioester bonds and/or nucleotide analogues, commonly used in oligonucleotide anti-sense approaches. Said modifications may be useful for the stabilization of the nucleic acid molecule against endo- and/or exonucleases in the cell. Said nucleic acid molecules may be transcribed by an appropriate vector containing a chimeric gene which allows for the transcription of said nucleic acid molecule in the cell. Such nucleic acid molecules may further contain ribozyme sequences which specifically cleave the (pre)-mRNA comprising the nucleic acid molecule of the invention. Furthermore, oligonucleotides can be designed which are complementary to a nucleic acid molecule of the invention (triple helix; see Lee, Nucl. Acids Res. 6 (1979), 3073; Cooney, Science 241 (1988), 456 and Dervan, Science 251 (1991), 1360), thereby preventing transcription and the production of the encoded oligopeptide.

The present gene can be obtained, for example, by the following method.

The tissues of a leguminous plant such as broad bean (*Vicia faba*) or soybean (*Glycine max*) are frozen in liquid nitrogen and ground physically with a mortar or other means into finely powdered tissue debris. From the tissue debris, RNA is extracted by an ordinary method. Commercially available RNA extraction kits can be utilized in the extraction. The whole RNA is separated from the RNA extract by ethanol precipitation. From the whole RNA separated, poly-A tailed RNA is fractionated by an ordinary method. Commercially available oligo-dT columns can be utilized in the fractionation. cDNA is synthesized from the fraction obtained (i.e., poly-A tailed RNA) by an ordinary method. Commercially available cDNA synthesis kits can be utilized in the synthesis.

For example, cDNA fragments of the "raffinose synthetase gene having a nucleotide sequence coding for a protein having the amino acid sequence of SEQ ID NO:1" as the present gene can be obtained by PCR amplification using the broad bean-derived cDNA obtained above as a template and primers 1 to 3 shown in list 1 below. The primers used therein can be designed and synthesized on the basis of the nucleotide sequence of SEQ ID NO:2, depending upon the purpose. For example, in order to amplify the open reading frame region of the "raffinose synthetase gene having a nucleotide sequence coding for a protein having the amino acid sequence of SEQ ID NO:1," primers 1 to 4 shown in list 2 below may be designed and synthesized.

In the same manner, cDNA fragments of the "raffinose synthetase gene having a nucleotide sequence coding for

a protein having the amino acid sequence of SEQ ID NO:3" can be obtained by PCR amplification with the soybean-derived cDNA obtained above as a template and, for example, primers 4 to 6 shown in list 1 below. The primers used therein can be designed and synthesized on the basis of the nucleotide sequence of SEQ ID NO:4, depending upon the purpose. For example, in order to amplify the open reading frame region of the "raffinose synthetase gene having a nucleotide sequence coding for a protein having the amino acid sequence of SEQ ID NO:3," primers 5 to 8 shown in list 2 below may be designed and synthesized.

The amplified DNA fragments can be subcloned according to ordinary methods, for example, as described in "Molecular Cloning: A Laboratory Manual 2nd edition" (1989), Cold Spring Harbor Laboratory Press; and "Current Protocols In Molecular Biology" (1987), John Wiley & Sons, Inc. ISBN 0-471-50338-X. More specifically, cloning can be effected, for example, using a TA cloning kit (Invitrogen) and a plasmid vector such as pBluescript II (Stratagene). The nucleotide sequences of the DNA fragments cloned can be determined by the dideoxy terminating method, for example, as described by F. Sanger, S. Nicklen, A.R. Coulson, Proceedings of National Academy of Science U.S.A. (1977), 74, pp. 5463-5467. For example, ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit commercially available from Perkin-Elmer may preferably be used.

(List 1)

Primer 1: AATTTTCAAG CATAGCCAAG TTAACCACT 30 mer
 Primer 2: GCTCACAAGA TAATGATGTT AGTC 24 mer
 Primer 3: ATACAAGTGA GGAACCTGAC CA 22 mer
 Primer 4: CCAAACCATTA GCAAACCTAA GCAC 24 mer
 Primer 5: ACAACAGAAA AATATGACTC TTATTACT 28 mer
 Primer 6: AAAAGAGAGT CAAACATCAT AGTATC 26 mer

(List 2)

Primer 1: ATGGCACCAC CAAGCATAAC CAAAACCTGC 29 mer
 Primer 2: ATGGCACCAC CAAGCATAAC CAAAACCTGCA ACCCTCCAAG ACG 43 mer
 Primer 3: TCAAAATAAA AACTGGACCA AAGAC 25 mer
 Primer 4: TCAAAATAAA AACTGGACCA AAGACAATGT 30 mer
 Primer 5: ATGGCTCCAA GCATAAGCAA AACTG 25 mer
 Primer 6: ATGGCTCCAA GCATAAGCAA AACTGTGGAA CT 32 mer
 Primer 7: TCAAAATAAA AACTCAACCA TTGAC 25 mer
 Primer 8: TCAAAATAAA AACTCAACCA TTGACAATTT TGAAGCACT 39 mer

The term "gene fragment" as used herein refers to a gene fragment having a partial nucleotide sequence of the present gene (hereinafter referred to simply as the present gene fragment). For example, it may be a gene fragment derived from a plant and having a partial nucleotide sequence of the gene having a nucleotide sequence coding for a protein capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. Specific examples of the present gene fragment are a gene fragment having a partial nucleotide sequence of the gene having a nucleotide sequence coding for the amino acid sequence of SEQ ID NO:1 and a gene fragment having a partial nucleotide sequence of the gene having a nucleotide sequence of SEQ ID NO:2, more specifically a gene fragment having a nucleotide sequence or a partial nucleotide sequence thereof, coding for any of the amino acid sequences shown in list 3 below.

These gene fragments can be used as probes in the hybridization method or as primers in the PCR method. For the primers in the PCR method, it is generally preferred that the number of nucleotides is greater from a viewpoint that the specificity of annealing is ensured; it is, however, also preferred that the number of nucleotides is not so great from viewpoints that the primers themselves are liable to have a higher structure giving possible deterioration of the annealing efficiency and that complicated procedures are required in the purification after the synthesis. In usual cases, preferred is a gene fragment consisting of single-stranded DNA, wherein the number of nucleotides is in the range of from 15 to 50.

(List 3)

#1 Gly Ile Lys Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly
 #2 Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr
 #3 Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly Trp Gln

#4 Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr Glu Glu Asn
 #5 Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly Gly Val Arg Pro
 #6 Thr Met Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val Pro Pro
 #7 Gly Leu His Ser His Leu Glu Ser Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu
 #8 Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu
 #9 Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala
 #10 Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser
 Asp Pro Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys
 #11 Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu
 Phe His Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp
 #12 Leu Pro Asp Gly Ser Ile Leu Arg Cys
 #13 Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp Asn
 #14 Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp
 #15 Phe Ala Pro Ile Gly Leu Val Asn Met

The present gene fragment is labeled, and then used as a probe in the hybridization method and hybridized to organism-derived DNA, so that a DNA fragment having the probe specifically bound thereto can be detected. Thus, from an organism-derived gene library, a raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of an enzyme capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule; or a gene fragment having a partial nucleotide sequence thereof, can be detected (hereinafter referred to simply as the present detection method).

As the organism-derived DNA, for example, a cDNA library or a genomic DNA library of a desired plant can be used. The gene library may also be a commercially available gene library as such or a library prepared according to an ordinary library preparation method, for example, as described in "Molecular Cloning: A Laboratory Manual 2nd edition" (1989), Cold Spring Harbor Laboratory Press; "Current Protocols In Molecular Biology" (1987), John Wiley & Sons, Inc. ISBN 0-471-50338-X.

As the hybridization method, plaque hybridization or colony hybridization can be employed, depending upon the kind of vector used in the preparation of a library. More specifically, when a library to be used is constructed with a phage vector, a suitable host microorganism is mixed with the phage under infectible conditions, which is further mixed with a soft agar medium, and the mixture is plated on an agar medium. Thereafter, a culture is grown at 37°C until a plaque of an appropriate size appears. When a library to be used is constructed with a plasmid vector, the plasmid is transformed in a suitable host microorganism to form a transformant. The transformant obtained is diluted to a suitable concentration, and the dilution is plated on an agar medium, after which a culture is grown at 37°C until a colony of an appropriate size appears.

In either case of the above libraries, a membrane filter is placed on the surface of the agar medium after the cultivation, so that the phage or transformant is transferred to the membrane. This membrane is denatured with an alkali, followed by neutralization, and for example, when a nylon membrane is used, the membrane is irradiated with ultraviolet light, so that DNA is fixed on the membrane. This membrane is then subjected to hybridization with the present gene fragment labeled by an ordinary method as a probe. For this method, reference may be made, for example, to D.M. Glover ed., "DNA cloning, a practical approach" IRL PRESS (1985), ISBN 0-947946-18-7. There are various reagents and temperature conditions to be used in the hybridization; for example, prehybridization is carried out by the addition of 6 x SSC (0.9 M NaCl, 0.09 M citric acid), 0.1-1% SDS, 100 µg/ml denatured salmon sperm DNA, and incubation at 65°C for 1 hour. The present gene fragment labeled is then added as a probe, and mixed. Hybridization is carried out at 42-68°C for 4 to 16 hours. The membrane is washed with 2 x SSC, 0.1-1% SDS, further rinsed with 0.2 x SSC, 0-0.1% SDS, and then dried. The membrane is analyzed, for example, by autoradiography or other techniques, to detect the position of the probe on the membrane and thereby detect the position of DNA having a nucleotide sequence homologous to that of the probe used. Thus, the present gene or the present gene fragment can be detected. The clone corresponding to the position of DNA thus detected on the membrane is identified on the original agar medium, and the positive clone is selected, so that the clone having the DNA can be isolated. The same procedures of detection are repeated to purify the clone having the DNA.

Other detection methods can also be used, for example, GENE TRAPPER cDNA Positive Selection System Kit commercially available from Gibco BRL. In this method, a single-stranded DNA library is hybridized with the present gene fragment biotinylated (i.e., probe), followed by the addition of streptavidin-bound magnet beads and mixing. From the mixture, the streptavidin-bound magnetic beads are collected with a magnet, so that single-stranded DNA having a nucleotide sequence homologous to that of the probe used, which has been bound to these beads through the present gene fragment, biotin and streptavidin, is collected and detected. Thus, the present gene or the present gene fragment can be detected. The single-stranded DNA collected can be changed into a double-strand form by treatment

with a suitable DNA polymerase using a suitable oligonucleotide as a primer.

The present detection method may also be used in the analysis of a plant. More specifically, plant genomic DNA is prepared according to an ordinary method, for example, as described in "Cloning and Sequence (Plant Biotechnology Experiment Manual)" compiled under the supervision of Itaru Watanabe, edited by Masahiro Sugiura, published by Noson Bunka-sha, Tokyo (1989). The plant genomic DNA is digested with several kinds of suitable restriction endonucleases, followed by electrophoresis, and the electrophoresed DNA is blotted on a filter according to an ordinary method. This filter is subjected to hybridization with a probe prepared from the present gene fragment by an ordinary method, and DNA fragments to which the probe hybridizes are detected. The DNA fragments detected are compared in length between different varieties of a specified plant species. The differences in length make possible the analysis of differences in phenotypic characteristics accompanied with the expression of raffinose family oligosaccharides between these varieties. Furthermore, when the DNA fragments detected by the above method are compared in length between the gene recombinant plant and the non-gene recombinant plant of the same variety, the former plant can be discriminated from the latter plant by the detection of hybridizing bands greater in number or higher in concentration for the former plant than for the latter plant. This method can be carried out according to the RFLP (restriction fragment length polymorphism) method, for example, as described in "Plant PCR Experiment Protocols" compiled under the supervision of Ko Shimamoto and Takuji Sasaki, published by Shujun-sha, Tokyo (1995), ISBN 4-87962-144-7, pp. 90-94.

The PCR method using a primer having the nucleotide sequence of the present gene fragment makes it possible to amplify from organism-derived DNA, a raffinose synthetase gene having a nucleotide sequence coding for the amino acid sequence of an enzyme capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule; or a gene fragment having a partial nucleotide sequence thereof (hereinafter referred to simply as the present amplification method).

More specifically, for example, an oligonucleotide having 15 to 50 nucleotides in the nucleotide sequence of the present gene fragment at the 3'-terminus is chemically synthesized by an ordinary synthesis method. Based on the codon table below, showing the correspondence of amino acids encoded in nucleotide sequences, a mixed primer can also be synthesized so that a residue at a specified position in the primer is changed to a mixture of several bases, depending upon the variation of codons which can encode a certain amino acid.

CODON TABLE							
Phe	UUU	Ser	UCU	Tyr	UAU	Cys	UGU
	UUC		UCC		UAC		UGC
Leu	UUA		UCA	Stop	UAA	Stop	UGA
	UUG		UCG		UAG		UGG
	CUU	Pro	CCU	His	CAU	Arg	CGU
	CUC		CCC		CAC		CGC
	CUA		CCA	Gln	CAA		CGA
	CUG		CCG		CAG		CGG
Ile	AUU	Thr	ACU	Asn	AAU	Ser	AGU
	AUC		ACC		AAC		AGC
	AUA		ACA	Lys	AAA	Arg	AGA
Met	AUG		ACG		AAG		AGG
Val	GUU	Ala	GCU	Asp	GAU	Gly	GGU
	GUC		GCC		GAC		GGC
	GUA		GCA	Glu	GAA		GGA
	GUG		GCG		GAG		GGG

Furthermore, a base capable of forming a pair with plural kinds of bases, such as inosine, can also be used instead

of the above mixture of several bases. More specifically, for example, primers having nucleotide sequences as shown in list 4 can be used. In this context, an oligonucleotide having the same nucleotide sequence as the coding strand of the present gene consisting of double-stranded DNA is designated "sense primer," and an oligonucleotide having a nucleotide sequence complementary to the coding strand, "antisense primer."

A sense primer having the same nucleotide sequence as present on the 5'-upstream side in the coding strand of a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof to be amplified, and an antisense primer having a nucleotide sequence complementary to the nucleotide sequence on the 3'-downstream side in this coding strand, are used in combination for PCR reaction to amplify a DNA fragment, for example, with a gene library, genomic DNA or cDNA as a template. At this time, the amplification of a DNA fragment can be confirmed by an ordinary method with electrophoresis. For the DNA fragment amplified, its restriction endonuclease map is constructed or its nucleotide sequence is determined by an ordinary method, so that the present gene or the present gene fragment can be identified. As the gene library used herein, for example, a cDNA library or a genomic cDNA library of a desired plant can be used. For the plant gene library, a commercially available library derived from plant can be used as such; or a library prepared according to an ordinary library preparation method, for example, as described in "Molecular Cloning: A Laboratory Manual 2nd edition" (1989), Cold Spring Harbor laboratory Press or "Current Protocols in Molecular Biology" (1987), John Wiley & Sons, Inc., ISBN 0-471-50338-X, can also be used. As the genomic DNA or cDNA used in the present amplification method, for example, cDNA or genomic cDNA prepared from a desired plant can be used.

More specifically, for example, a primer designed on the amino acid sequence of SEQ ID NO:1 is used for the present amplification method with cDNA derived from Japanese artichoke, which is a lamiaceous plant, as a template, so that a raffinose synthetase gene fragment having the nucleotide sequence of SEQ ID NO:6 can be amplified. Furthermore, for example, a primer designed on the amino acid sequence of SEQ ID NO:1 is used for the present amplification method with cDNA derived from corn, which is a gramineous plant, as a template, so that a raffinose synthetase gene fragment having the nucleotide sequence of SEQ ID NO:8 can be amplified.

(List 4)

1-F	32mer	TTIAAIGTITGGTGGACIACICAITGGGTIGG
2-F	41mer	ATIATIGAIAAITTIGGITGGTGIACITGGGAIGCITTITA
2-RV	41mer	TAIAAIGCITCCCAIGTICACCAICCAAIAITTITCIATAT
3-F	44mer	GGIGGITGICCCICGIGTITGTIATIGAIAGGIGTGGCA
3-RV	44mer	TGCCAICCITCITCIATATACIAAICCGIGGIGGICAICCICC
4-F	32mer	AAIAAICAITTTAAIGGIAAIGGIGTATIGC
4-RV	32mer	GCIATACICCCITTICCTTAAITGITTITT
5-F	38mer	TGGATGGGIAAITTIATICAICCGAITGGGAATGTT
5-RV	38mer	AACATITCCCAITCIGGITGIATIAAITTICCATCCA
6-RV	27mer	CATITTIACIA(AG)ICCIATIGGIGCIAA

The present amplification method can also be utilized for the analysis of a plant gene. More specifically, for example, plant genomic DNA prepared from different varieties of a specified plant species is used as a template for the present amplification method to amplify a DNA fragment. The DNA fragment amplified is mixed with a solution of formaldehyde, which is denatured by heating at 85°C for 5 minutes, followed by rapid cooling on ice. This sample is subjected to electrophoresis, for example, on a 6% polyacrylamide gel containing 0% or 10% glycerol. In this electrophoresis, a commercially available electrophoresis apparatus for SSCP (single strand conformation polymorphism) can be used, and electrophoresis is carried out, while the gel is kept at a constant temperature, e.g., 5°C, 25°C or 37°C. From the electrophoresed gel, a DNA fragment is detected, for example, by a method such as silver staining method with commercially available reagents.

From the differences of behavior between the varieties in the electrophoresis of the DNA fragment detected, a mutation in the raffinose synthetase gene is detected, and an analysis is carried out for differences caused by the muta-

tion in phenotypic characteristics accompanied with the expression of raffinose family oligosaccharides. This method can be carried out according to the SSCP method, for example, as described in "Plant PCR Experiment Protocols" compiled under the supervision of Ko Shimamoto and Takuji Sasaki, published by Shujun-sha, Tokyo (1995), ISBN 4-87962-144-7, pp. 141-146.

The present detection method or the present amplification method as described above can also be used for identifying a raffinose synthetase gene or a gene fragment having a partial nucleotide sequence thereof and then isolating and purifying the identified gene or gene fragment thereof to obtain the present gene (hereinafter referred to simply as the present gene acquisition method).

The present gene or the present gene fragment can be obtained, for example, by detecting a probe consisting of the present gene fragment hybridized to DNA in the organism-derived gene library by the present detection method as described above to identify DNA having a nucleotide sequence homologous with the probe used; purifying a clone carrying the DNA; and isolating and purifying plasmid or phage DNA from the clone. When the DNA thus obtained is a gene fragment having a partial nucleotide sequence of the raffinose synthetase gene, further screening of the gene library by the present gene detection method using the DNA as a probe gives the present gene in full length.

The present gene or the present gene fragment can be identified, for example, by effecting polymerase chain reaction using a primer having the nucleotide sequence of the present gene fragment to amplify a DNA fragment from the organism-derived DNA by the present amplification method as described above; and then constructing a restriction endonuclease map or determining a nucleotide sequence for the amplified DNA fragment. Based on the nucleotide sequence of the gene fragment obtained, an antisense primer is synthesized for the analysis of 5'-terminal sequences, and a sense primer is synthesized for the analysis of 3'-terminal sequences. The nucleotide sequence of the present gene in full length can be determined by the RACE method using these primers and a commercially available kit, e.g., Marathon Kit of Clontech. The present gene in full length can be obtained by synthesizing new primers based on both terminal sequences in the nucleotide sequence thus determined and effecting polymerase chain reaction again.

The present gene acquisition method as described above makes it possible to obtain raffinose synthetase genes as the present gene from various organisms. For example, a gene coding for a raffinose synthetase having an amino acid sequence that has about 50% or higher homology, in the region corresponding to the length of 400 or more amino acids, with the amino acid sequence of SEQ ID NO:1, and capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. More specifically, for example, a raffinose synthetase gene having the nucleotide sequence of SEQ ID NO:4 can be obtained by amplifying and identifying a DNA fragment containing a gene fragment having a partial nucleotide sequence of the raffinose synthetase gene by the present amplification method using primers designed from the amino acid sequence of SEQ ID NO:1 and soybean cDNA as a template; isolating and purifying the identified DNA fragment, followed by the above procedures to obtain a full-length gene containing the DNA fragment.

A chimera gene comprising the present gene and a promoter linked thereto (hereinafter referred to simply as the present chimera gene) can be constructed.

The promoter to be used is not particularly limited, so long as it is functionable in a host organism to be transformed. The promoter may include, for example, synthetic promoters functionable in *Escherichia coli*, such as *E. coli* lactose operon promoter, *E. coli* tryptophan operon promoter and *tac* promoter; yeast alcohol dehydrogenase gene (ADH) promoter, adenovirus major late (Ad.ML) promoter, SV40 early promoter, and baculovirus promoter.

When the host organism is a plant or a cell thereof, the promoter may include, for example, T-DNA derived constitutive promoters such as nopaline synthetase gene (NOS) promoter and octopine synthase gene (OCS) promoter; plant virus-derived promoters such as cauliflower mosaic virus (CaMV) derived 19S and 35S promoter; derived promoters such as phenylalanine ammonia-lyase (PAL) gene promoter, chalcone synthetase (CHS) gene promoter and pathogenesis-related protein (PR) gene promoter. Furthermore, vector pSUM-GY1 (see JP-A 06-189777/1994) can also be used, which has a promoter giving specific expression in a specified plant tissue, e.g., a promoter of soybean-derived seed storage protein glycinin gene. The use of a chimera gene constructed so as to have such a promoter makes it possible to increase or decrease the content of raffinose family oligosaccharides in a specified tissue of a plant.

The present chimera gene is then introduced into a host organism according to an ordinary gene engineering method to give a transformant. If necessary, the present chimera gene may be used in the form of a plasmid, depending upon the transformation method for introducing the gene into the host organism. Furthermore, the present chimera gene may contain a terminator. In this case, it is generally preferred that the chimera gene is constructed so as to have a terminator downstream the raffinose synthetase gene. The terminator to be used is not particularly limited, so long as it is functionable in a host organism to be transformed. For example, when the host organism is a plant or a cell thereof, the terminator may include, for example, T-DNA derived constitutive terminators such as nopaline synthetase gene (NOS) terminator; and plant derived terminators such as terminators of allium virus GV1 or GV2.

If necessary, the present gene may be used in the form of a plasmid. For example, when the host organism is a microorganism, the plasmid constructed is introduced into the microorganism by an ordinary means, for example, as described in "Molecular Cloning: A Laboratory Manual 2nd edition" (1989), Cold Spring Harbor laboratory Press or

"Current Protocols in Molecular Biology" (1987), John Wiley & Sons, Inc., ISBN 0-471-50338-X. The microorganism thus transformed is selected with a marker such as antibiotic resistance or auxotrophy. When the host organism is a plant, the plasmid constructed is introduced into a plant cell by an ordinary means such as infection with *Agrobacterium* (see JP-B 2-58917/1990 and JP-A 60-70080/1985), electroporation into protoplasts (see JP-A 60-251887/1985 and JP-B 5-68575/1993) or particle gun method (see JP-A 5-508316/1993 and JP-A 63-258525/1988). The plant cell transformed by the introduction of a plasmid is selected with an antibiotic such as kanamycin or hygromycin. From the plant cell thus transformed, a transformed plant can be regenerated by an ordinary plant cell cultivation method, for example, as described in "Plant Gene Manipulation Manual (How to Produce Transgenic Plants)" written by Uchimiya, 1990, Kodan-sha Scientific (ISBN 4-06-153513-7), pp. 27-55. Furthermore, the collection of seeds from the transformed plant also makes it possible to proliferate the transformed plant. In addition, crossing between the transformed plant obtained and the non-transformed plant makes it possible to produce progenic plants with the character of the transformed plant.

The content of raffinose family oligosaccharides can be changed by introducing the present gene into a host organism or a cell thereof, and modifying the metabolism in the host organism or the cell thereof. As such a method, for example, there can be used a method for metabolic modification to increase the amount of raffinose family oligosaccharides in a host organism or a cell thereof by constructing the present chimera gene comprising the present gene and a promoter linked thereto, in which case the present gene is linked to the promoter in an original direction suitable for transcription, translation, and expression as a protein, and then introducing the present chimera gene into the host organism or the cell thereof; or a method for metabolic modification to decrease the amount of raffinose family oligosaccharides in a host organism or a cell thereof by constructing the present chimera gene comprising the present gene and a promoter linked thereto, in which case the present gene is linked to a promoter in a reverse direction unsuitable for translation and expression as a protein, and then introducing the present chimera gene into the host organism or the cell thereof.

The term "raffinose synthetase protein" as used herein refers to a protein encoded in the present gene (hereinafter referred to simply to the present protein). For example, it may include an enzyme protein having the amino acid sequence of SEQ ID NO:1 or SEQ ID NO: 3, or having an amino acid sequence derived by deletion, replacement, modification or addition of one or several amino acids in the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:3; and capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule.

Specific examples of the present protein are an enzyme protein having the amino acid sequence of SEQ ID NO:1 (799 amino acids; molecular weight, 89 kDa) and an enzyme protein having the amino acid of SEQ ID NO:3 (781 amino acids; molecular weight, 87 kDa).

The present protein, although it can be prepared, for example, from leguminous plants such as broad bean (*Vicia faba*), by an ordinary biochemical method such as $(\text{NH}_4)_2\text{SO}_4$ precipitation, ion exchange column, hydrophobic column, hydroxyapatite column or gel filtration column, can also be prepared from the host organism transformed with the present plasmid, or a cell thereof. More specifically; for example, using GST Gene Fusion Vectors Kit of Pharmacia, the present gene is inserted into an expression vector plasmid attached to the Kit. The resulting vector plasmid is introduced into a microorganism such as *E. coli* according to an ordinary gene engineering method. A culture of the transformant obtained is grown on a medium with the addition of IPTG (isopropylthio- β -D-galactoside), so that the present protein can be expressed and derived as a fused protein in the culture. The fused protein expressed and induced can be isolated and purified by an ordinary method such as disruption of bacterial cells, column operation or SDS-PAGE electrophoresis. The digestion of the fused protein with a protease such as thrombin or blood coagulation factor Xa gives the present protein. This may preferably be made, for example, according to the method described in "Current Protocols In Protein Science" (1995), John Wiley & Sons, Inc. ISBN 0-471-11184-8. The activity of the present protein can be measured, for example, by the method described in L. Lehle and W. Tanner, Eur. J. Biochem., 38, 103-110 (1973).

An anti-raffinose synthetase antibody capable of binding to a raffinose synthetase protein (hereinafter referred to simply as the present antibody) can be produced by an ordinary immunological method using the present protein prepared above, as an antigen. More specifically, the present antibody can be produced, for example, according to the method described in Ed Harlow and David Lane, "Antibodies: A Laboratory Manual" (1988), Cold Spring Harbor Laboratory Press, ISBN 0-87969-314-2.

The present protein can be detected by treating test proteins with the present antibody and detecting a protein having the present antibody bound specifically thereto. Such a detection method can be carried out according to an immunological technique such as Western blot method or enzyme-linked immunosorbent assay (ELISA), for example, as described in Ed Harlow and David Lane, "Antibodies: A Laboratory Manual" (1988), Cold Spring Harbor Laboratory Press.

The Western blot method is carried out, for example, as follows: Proteins are extracted from a plant, for example, according to the method described in Methods in Enzymology, volume 182, "Guide to Protein Purification," pp. 174-193, ISBN 9-12-182083-1. The composition of an extraction buffer can suitably be changed depending upon the plant tissue

used. The proteins extracted are electrophoresed according to an ordinary SDS-PAGE method. The proteins electrophoresed in the gel are transferred to a membrane by Western blotting with an ordinary electrical method. More specifically, for example, the gel is immersed in a transfer buffer (25 mM Tris, 192 mM glycine, 20% methanol) for 10 minutes, and then placed onto a PVDF membrane cut into the same size as that of the gel. The gel together with the membrane is set in a commercially available transfer apparatus of the semi-dry type. Blotting is carried out at a constant current of 0.8 to 2 mA/cm² for 45 minutes to 1 hour. The proteins transferred to the membrane can be detected immunologically with a kit for Western blot detection using a primary antibody, and a secondary antibody or protein A, which has been labeled with alkaline phosphatase or horseradish peroxidase. At this time, the present protein on the membrane can be detected by the use of the present antibody as a primary antibody.

In the ELISA method, for example, the property of proteins binding to the surface of a 96-well ELISA plate made of a resin is utilized in principle for the immunological detection of an antigen finally bound to the surface of the ELISA plate. The test proteins are added as a solution and bound to an ELISA plate, followed by blocking, for example, by the addition of PBS containing a protein such as 5% bovine serum albumin. Thereafter, the well is washed with PBS, to which a solution containing the present antibody is added to effect the reaction. After the well is washed, a solution containing a secondary antibody labeled with alkaline phosphatase or horseradish peroxidase is further added to the well, followed by washing. Finally, a substrate solution for detection is added to the well, and the color development of the substrate is detected with an ELISA reader.

In another method, the present antibody is added and bound to an ELISA plate, followed by blocking, for example, by the addition of PBS containing a protein such as 5% bovine serum albumin. The test proteins are then added as a solution, and an antigen contained in the test proteins is bound to the present antibody that has been bound to the plate, followed by washing, and the present antibody is further added to the well. The present antibody used at this time is preferably one prepared from an animal species different from that used for the preparation of the present antibody used first. A solution containing a secondary antibody labeled with alkaline phosphatase or horseradish peroxidase is then added to the well, followed by washing. The secondary antibody used at this time must have the property of binding to the present antibody added later. Finally, a substrate solution for detection is added, and the color development is detected with an ELISA reader.

Examples

The present invention will be further illustrated by the following examples; however, the present invention is not limited to these examples in any way whatsoever.

Example 1 (Purification of Galactinol)

About 250 ml of sugar beet blackstrap molasses was five-fold diluted with methanol. The dilution was centrifuged at 21,400 x g for 15 minutes at room temperature to remove insoluble matter. The supernatant obtained was transferred into a 2-liter Erlenmeyer flask, to which isopropanol at a half volume was added portionwise with stirring. The flask was left at room temperature for a while until the resulting precipitate adhered to the wall of the flask. The supernatant was then discarded by decantation. To the precipitate was added 500 ml of ethanol, and the mixture was washed by stirring with a rotary shaker. The washing was further repeated several times. The washed precipitate was scraped off from the wall of the flask, followed by air drying on a filter paper. The air-dried precipitate (dry powder) was dissolved in purified water to about 40% (w/v). To this solution was added AG501-X8(D) of BioRad, followed by stirring. This operation was repeated until the color of the solution became almost unobserved. The resulting solution was treated with a Sep-Pak QMA column of Millipore, and further pretreated with Sep-Pak CM, Sep-Pak C18 and Sep-Pak Silica columns of Millipore. The resulting solution was loaded at a volume of 5 ml onto a column of Wako-gel LP40C18 (Wako Pure Chemical Industries, 2.6 cm x 85 cm), and eluted with purified water. The sugar content of the eluate was measured with a portable sugar refractometer, and the sugar composition was analyzed by high performance liquid chromatography (HPLC) with a Sugar-pak Na (7.8 mm x 300 mm) column of Millipore. The detection of sugars was carried out with model 410 Differential Refractometer of Waters. The eluate containing galactinol was lyophilized, and the resulting lyophilized powder was dissolved in 5 ml of purified water. The solution was loaded onto a column of TOYOPEARL HW40(S) (Toso, 2.6 cm x 90 cm), and eluted with purified water. The eluate was analyzed in the same manner as described above, so that purified galactinol was obtained.

The galactinol obtained was kept at 25°C for 40 minutes in the reaction mixture that came to contain 80 mM phosphate buffer (pH 6.5), 2 mg/ml galactinol, and 8.3 U α -galactosidase (Boehringer Mannheim, *E. coli* overproducer 662038). The reaction mixture was extracted with chloroform, and the water layer was analyzed by HPLC. The resulting galactinol was confirmed to be hydrolyzed into galactose and myo-inositol.

Example 2 (Measurement of Raffinose Synthase Activity)

The raffinose synthetase activity was measured under the following conditions according to the description of L. Lehle and W. Tanner, *Eur. J. Biochem.*, 38, 103-110 (1973).

First, 2 μ l of a sample to be used in the measurement of activity was added to 18 μ l of the reaction mixture that came to contain 100 mM Tris-HCl (pH 7.4), 5 mM DTT (dithiothreitol), 0.01% BSA, 200 μ M sucrose, 5 mM galactinol, 740 KBq/ml (31.7 μ M) [14 C] sucrose, and the reaction mixture was kept at 37°C for 3 to 20 hours. After the reaction, 30 μ l of ethanol was added to the reaction mixture, followed by stirring and centrifugation at 15,000 rpm for 5 minutes. The supernatant was spotted at a volume of 5 μ l on an HPTLC plate of cellulose for thin layer chromatography (Merck, 10 cm x 20 cm), and developed with n-butanol : pyridine : water : acetic acid = 60 : 40 : 30 : 3. The developed plate was dried and then quantitatively analyzed with an imaging analyzer (Fuji Photographic Film, FUJIX Bio Imaging Analyzer BAS-2000II) for the determination of [14 C] raffinose produced.

Example 3 (Purification of Raffinose Synthase)

The purification of raffinose synthetase from broad bean was carried out as follows: For each purified protein solution, proteins present in the protein solution were analyzed by SDS-PAGE (Daichi Kagaku Yakuhin), and the enzyme activity thereof was measured according to the method described in Example 2.

First, 300 g of immature seeds of broad bean (Nintoku Issun) stored at -80°C was thawed and then peeled. The peeled seeds were put in 600 ml of 100 mM Tris-HCl (pH 7.4), 5 mM DTT (dithiothreitol), 1 mM EDTA, 1 mM PMSF (phenylmethylsulfonyl fluoride) and 1 mM benzamide, and ground on ice with a mortar. The ground material was centrifuged at 21,400 x g for 50 minutes at 4°C. To the resulting supernatant was added 10% polyethylene imine (pH 8.0) at a 1/20 volume. The mixture was stirred at 4°C for 15 minutes, and centrifuged at 15,700 x g for 20 minutes at 4°C. To the resulting supernatant was added 196 g/l of $(\text{NH}_4)_2\text{SO}_4$ with stirring. The mixture was stirred in ice for 30 minutes, and centrifuged at 15,700 x g for 20 minutes at 4°C. To the resulting supernatant was further added 142 g/l of $(\text{NH}_4)_2\text{SO}_4$ with stirring. After the stirring in ice for 30 minutes, the mixture was centrifuged at 15,700 x g for 20 minutes at 4°C. The resulting precipitate was dissolved in 50 ml of 100 mM Tris-HCl (pH 7.4) and 5 mM DTT (dithiothreitol), and the solution was dialyzed against 20 mM Tris-HCl (pH 7.4), 1 mM DTT (dithiothreitol) and 1 mM EDTA at 4°C overnight. After the dialysis, the suspension was centrifuged at 70,000 x g for 60 minutes at 4°C. To the resulting supernatant was added 1 mM benzamidinium \cdot HCl, 5 mM ϵ -amino-n-caproic acid, 1 μ g/ml antipain, 1 μ g/ml leupeptin and 10 mM EGTA, and 2 M KCl was further added portionwise at a 1/40 volume. The mixture was loaded onto a column of DEAE-Sepharcel (Pharmacia, 2.5 cm x 21.5 cm) equilibrated with 0.05 M KCl, 20 mM Tris-HCl (pH 7.4), 1 mM DTT (dithiothreitol) and 1 mM EDTA, and the adsorbed proteins were eluted with a gradient of 0.05 to 0.5 M KCl. The purification steps up to this stage were repeated three times, and fractions having raffinose synthase activity were combined and then purified as follows:

To the eluted fraction having raffinose synthetase activity was added portionwise saturated $(\text{NH}_4)_2\text{SO}_4$ at a 1/4 volume. The solution was loaded onto a column of Phenyl-Sepharose (Pharmacia, 2.5 cm x 10.2 cm) equilibrated with 20% saturated $(\text{NH}_4)_2\text{SO}_4$, 20 mM Tris-HCl (pH 7.4), 1 mM DTT (dithiothreitol) and 1 mM EDTA, and the adsorbed proteins were eluted with a gradient of 20% to 0% $(\text{NH}_4)_2\text{SO}_4$. The resulting active fraction was diluted by the addition of 0.01 M potassium phosphate buffer (pH 7.5) at a 2-fold volume. The diluted solution was loaded onto a column of Econo-Pac 10DG (BioRad, 5 ml) previously equilibrated with 0.01 M potassium phosphate buffer (pH 7.5) and 2 mM DTT (dithiothreitol), and the adsorbed proteins were eluted with a gradient of 0.01 to 0.5 M potassium phosphate buffer (pH 7.5) and 2 mM DTT (dithiothreitol). The active fraction obtained at this stage was found to have been purified up to 6500-fold or higher specific activity. Part of the resulting purified protein solution having raffinose synthetase activity was loaded onto a column of Superdex 200 (Pharmacia, 1.6 cm x 60 cm) equilibrated with 0.2 M KCl, 20 mM Tris-HCl (pH 7.4), 1 mM DTT (dithiothreitol) and 1 mM EDTA. The purified proteins thus separated were subjected to SDS-PAGE, and the raffinose synthetase activity was measured. A protein band having raffinose synthetase activity was identified as having a molecular weight of about 90 kDa on the SDS-PAGE.

Example 4 (Analysis of Partial Amino Acid Sequence of Raffinose Synthase)

To about 1 ml of the purified protein solution, which had been purified with a column of Econo-Pac 10DG (BioRad, 5 ml) in Example 3, was added 100% TCA at a 1/9 volume, and the mixture was left on ice for 30 minutes. After centrifugation at 10,000 x g for 15 minutes, the resulting precipitate was suspended in 500 μ l of cold acetone (-20°C), followed by further centrifugation. This acetone washing was repeated, and the collected precipitate was dried and then dissolved in 200 μ l of SDS-sample buffer, followed by SDS-PAGE. CBB staining was effected for the electrophoresed gel, from which the band of a raffinose synthetase protein was cut out.

To the gel thus taken was added 1 ml of 50% acetonitrile and 0.2 M ammonium carbonate (pH 8.9), and washing

was continued with stirring at room temperature for 20 minutes. The gel was washed once again in the same manner, and dried under reduced pressure to an extent giving a volume reduction. To this gel was 1 ml of 0.02% Tween-20 and 0.2 M ammonium carbonate (pH 8.9), and the mixture was stirred at room temperature for 15 minutes. After removal of the solution, 400 μ l of 8 M urea and 0.4 M NH_4HCO_3 was added, to which 40 μ l of 45 mM DTT (dithiothreitol) was further added, and the mixture was left at 50°C for 20 minutes. After complete return to room temperature, 4 μ l of 1 M iodoacetic acid was added, and the mixture was stirred in the dark at room temperature for 20 minutes. After removal of the solution, 1 ml of purified water was added, and the mixture was stirred at room temperature for 5 minutes, followed by washing. After further two washings, 1 ml of 50% acetonitrile and 0.2 M ammonium carbonate (pH 8.9) was added, and the mixture was stirred at room temperature for 15 minutes. The same treatment was repeated once again, after which the solution was removed, and the gel was dried under reduced pressure to an extent giving a volume reduction.

To this gel was added a solution of Achromobacter Protease I (Takara, Residue-specific Protease Kit) at a volume of 100 μ l. Further added was 0.02% Tween-20 and 0.2 M ammonium carbonate (pH 8.9) to an extent that the gel was not exposed from the surface of the solution, and the mixture was left at 37°C for 42 hours. Further added was 500 μ l of 0.09% TFA and 70% acetonitrile, and the mixture was stirred at room temperature for 30 minutes. The resulting mixture as contained in a sample tube was floated in an ultrasonic bath, followed by ultrasonic treatment (BRANSON, 60 W output power) for 5 minutes. The tube and contents thus treated were centrifuged, and the resulting extract was collected in another silicone-coated sample tube. On the other hand, 500 μ l of 0.09% TFA and 70% acetonitrile was added again to the precipitate, followed by repeated extraction in the same manner as described above. The resulting extracts were combined and then concentrated under reduced pressure to an extent giving a solution remained at a volume of 200 to 300 μ l. To the concentrate was added 25 μ l of 8 M urea and 0.4 M NH_4HCO_3 , and the mixture was concentrated to an extent giving a solution remained at a volume of 100 μ l or lower. The concentrate was brought to about 100 μ l with purified water, and the mixture was filtered through a filter of Ultrafree C3 GV (Millipore). The filtrate obtained was then subjected to elution through a column of Aquapore BU-300 C-4 (2.1 mm x 300 mm) by a gradient of 0.1% TFA/2.1% to 68.6% acetonitrile. Absorbance at 215 nm was monitored to collect a fraction at a peak thereof. The sample collected was evaporated under reduced pressure to complete dryness, and then analyzed with a Protein Sequencer 473A of ABI to determine a partial amino acid sequence of a raffinose synthetase.

Example 5 (Preparation of cDNA)

About 2 g of immature seeds of broad bean (Nintoku Issun) was frozen in liquid nitrogen and then ground with a mortar, to which 20 ml of Isogen (Nippon Gene) was added, and the mixture was further thoroughly ground. The ground material was transferred into a centrifugation tube, to which 4 ml of chloroform was added, and the mixture was stirred with a vortex mixer and then centrifuged at 6,500 x g for 10 minutes at 4°C. The water layer was collected, to which 10 ml of isopropanol was added, and the mixture was stirred and then centrifuged at 6,500 x g for 10 minutes at 4°C. The resulting precipitate was washed with 10 ml of 70% ethanol and then dissolved in 1 ml of elution buffer (10 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.1% SDS). The solution was left at 60°C for 10 minutes and then centrifuged at 10,000 x g for 1 minute to remove insoluble matter. To the resulting supernatant was added an equivalent volume of Oligotex-dT30 (Takara), and the mixture was stirred and then left at 65°C for 5 minutes. The mixture was placed on ice and then left for 3 minutes, to which 200 μ l of 5 M NaCl was added, and the mixture was left at 37°C for 10 minutes. The mixture was then centrifuged at 10,000 x g at 4°C for 3 minutes. The precipitate was collected and then suspended in 1 ml of TE buffer, and the suspension was left at 65°C for 5 minutes, which was placed on ice and then left for 3 minutes, followed by centrifugation at 10,000 x g for 3 minutes at 4°C to remove the precipitate.

To the resulting supernatant were added 100 μ l of 3 M sodium acetate and 2 ml of ethanol, and RNA was ethanol precipitated and collected. The collected RNA was washed twice with 70% ethanol and then dissolved in 20 μ l of sterilized water, which was used for the subsequent cDNA synthesis. The amount of RNA obtained was determined by the measurement of absorbance at 260 nm.

For the cDNA synthesis, First Strand Synthesis Kit for RT-PCR (Amercham) and cDNA Synthesis Kit (Takara) were used, and all operations were made according to the protocol.

Example 6 (Nucleotide sequence Analysis of Raffinose Synthase Gene from cDNA)

Based on the amino acid sequence obtained in Example 4, mixed synthetic DNA primers having the nucleotide sequences shown in list 5 below were synthesized. The PCR method was carried out with Gene Amp PCR Systems 2400 and DNA Thermal Cycler Model 480 of Perkin-Elmer using Advantage KlenTaq cDNA Kit of Clontech. The polymerase chain reaction was effected with the above primers at 94°C for 1 minute, at 50°C for 3 minutes, and at 72°C for 3 minutes, and this reaction was repeated forty times. As a result, the combinations of primers 8.2 and 13.3RV, primers 13.4 and 10.3RV, and primers 7.4 and 10.3RV, having the nucleotide sequences shown in list 5 below, gave an

amplification of 1.2 kb, 0.5 kb, and 1.2 kb bands, respectively. These amplified DNA fragments were cloned with a TA cloning kit (Invitrogen), followed by sequence reaction using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit of Perkin-Elmer and nucleotide sequence analysis with a 373S DNA sequencer of ABI. As a result, these DNA fragments were found to have a nucleotide sequence extending from base 813 to base 1915, base 1936 to base 2413, and base 1226 to base 2413, respectively, in the nucleotide sequence of SEQ ID NO:2. Based on these nucleotide sequences, synthetic DNA primers having nucleotide sequences shown in list 6 below were prepared, and the nucleotide sequences in both terminal regions of cDNA were analyzed with Marathon cDNA Amplification Kit of Clontech. As a result, the nucleotide sequence of SEQ ID NO:2 was finally determined.

(List 5)

#8.2 26mer
AA(AG) AC(ATGC) GC(ATGC) CC(ATGC) AG(TC) AT(TCA) AT(TCA) GAC AA

#13.4 20mer
AA(AG) AT(TCA) TGG AA(TC) CT(ATGC) AAC AA

#7.4 24mer
AA(AG) GC(ATGC) AG(AG) GT(ATGC) GT(ATGC) GT(ATGC) CC(ATGC) AAG

#13.3RV 21mer
(TC)TT (AG)TT (ATGC)AG (AG)TT CCA (AGT)AT TTT

#10.3RV 21mer
(TC)TT (AG)TC (TC)TC (AG)TA (ATGC)AG (AG)AA TTT

(List 6)

RS-2RV 30mer
GGCTGAGGTTTCGGTTCATTCTGAATCATC

RS-7 30mer
CCAAATGGTACATATTGGCTCCAAGGTTGT

RS-8 30mer
AAGAGTGTATCTGAATTTTCACGCGCGGTG

RS-9 30mer
TGGTGCAATGGGAAAACCTCCAATGAGCACC

RS-10 30mer
ATGAAGTGTCTGATAGATTGAAAGTTTCG

RS-11 30mer
CAGTCTCTGGAGTTTGATGATAATGCAAGT

Example 7 (Cloning of Raffinose Synthetase Gene from Broad Bean cDNA)

The primers designed from the amino acid sequence of SEQ ID NO:1, i.e., primers having nucleotide sequences shown in list 7 below, were synthesized. Using these primers and cDNA obtained in Example 5 as a template, a DNA fragment of the open reading frame region was amplified by PCR under the conditions described in Example 6. The amplified DNA fragment was digested with the restriction endonucleases *Bam* HI and *Xba* I whose recognition sequences were contained in the primers used. Using Ligation Kit (Takara), the DNA fragment thus digested was cloned in the plasmid pBluescriptII KS- (Stratagene) previously digested with *Bam* HI and *Xba* I. The nucleotide sequence of the cloned DNA fragment was confirmed with ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit of Perkin-Elmer. In the clone thus obtained, it was found that the base at position 1591 in the nucleotide sequence of SEQ ID NO:2 had been changed from thymine (T) to cytosine (C). This was, however, a nonsense mutation without a change of the amino acid; therefore, this clone was designated pBluescriptKS-RS, and used in the subsequent experiment.

(List 7)

RS-N 41mer
CGCGGATCCACCATGGCACCACCAAGCATAACCAAACTGC

RS-C 37mer
TGCTCTAGATTATCAAATAAAACTGGACCAAAGAC

Example 8 (Expression of Broad Bean Raffinose Synthetase Gene in *E. coli*)

The plasmid pBluescriptKS-RS having the broad bean raffinose synthetase gene obtained in Example 7 was digested with *Bam* HI and *Not* I, and cloned in the plasmid pGEX-4T3 (Pharmacia) digested with *Bam* HI and *Not* I to give the plasmid pGEX-RS as shown in Figure 1.

The plasmid pBluescriptKS-RS was digested with *Nco* I and *Xba* I, and cloned in the plasmid pTrc99A (Pharmacia) digested with *Nco* I and *Xba* I to give the plasmid pTrc-RS as shown in Figure 1.

These plasmids were introduced into *E. coli* strain HB101, and the resulting transformants were used for the confirmation of raffinose synthetase expression. Overnight cultures of the transformants were inoculated at a volume of 1 ml each into 100 ml of LB medium and incubated at 37°C for about 3 hours, followed by the addition of IPTG (isopropylthio- β -D-galactoside) to a final concentration of 1 mM and further incubation for 5 hours. The cultures were centrifuged at 21,400 x g for 10 minutes, and the bacterial cells were collected. The collected bacterial cells were stored at -80°C. To the frozen bacterial cells was added a 10-fold volume of 100 mM Tris-HCl (pH 7.4), 1 mM EDTA, 5 mM DTT (dithiothreitol), 1 mM PMSF (phenylmethylsulfonyl fluoride) and 1 mM benzamide, and the bacterial cells were thawed and suspended. These suspensions were treated with an ultrasonic disrupter (Branson) to effect the disruption of the bacterial cells. The disrupted cell mixtures obtained were centrifuged at 16,000 x g for 10 minutes, and soluble protein solutions were collected.

The protein solutions thus obtained were used at a volume of 4 μ l each for the measurement of raffinose synthetase activity according to the method described above. The reaction was effected at 37°C for 64 hours. As a control, *E. coli* strain HB101 that had been transformed with one of the vectors, pGEX-4T3, was used. The results are shown in Table 1. The synthesis of raffinose was detected in the samples from the transformants HB101 (pGEX-RS) and HB101 (pTrc-RS).

TABLE 1

Transformant	Amount of raffinose produced (pmol)
HB101 (pGEX4T-3)	0.56
HB101 (pGEX-RS)	10.50
HB101 (pTrc-RS)	11.10

Example 9 (Cloning of Raffinose Synthetase Gene from Soybean cDNA)

In the same manner as described in Example 5, cDNA was obtained from immature seeds of soybean (*Glycine max*) Williams 82. Using this cDNA as a template and primers designed from the amino acid sequence of SEQ ID NO:1, i.e., primers having nucleotide sequences shown in list 8 below, a DNA fragment was amplified by PCR under the conditions described in Example 6. The DNA fragment thus amplified by PCR was cloned with a TA cloning kit (Invitrogen), followed by sequence reaction using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit of Perkin-Elmer and nucleotide sequence analysis with a 373S DNA sequencer of ABI. Based on this sequence, primers having nucleotide sequences shown in list 9 below were synthesized. The synthesis of cDNA was carried out with Marathon Kit of Clontech using mRNA obtained in the same manner as described in Example 5 from leaves of soybean Williams 82. The cDNA obtained was ligated to an adaptor contained in this kit with ligase. This operation was made according to the protocol attached. Using the adaptor-ligated cDNA thus prepared, polymerase chain reaction was effected with the primers shown in list 9 below. The nucleotide sequences in both terminal regions of the gene were analyzed according to the protocol attached to the Marathon Kit of Clontech. As a result, the nucleotide sequence of SEQ ID NO:4 was determined.

(List 8)

- 1-F primer 35mer
CGATTIAAIGTITGGTGGACIACICAITGGGTIGG
- 2-RV primer 45mer
GGCCTAIAAIGCITCCAIGTICACCAICCAIAITTITCIAT
- 5-F primer 41mer
CGATGGATGGGIAAITTATICAICCAITGGGAIATGTT
- 6-RV primer 32mer

GGCCACATITTTIACIA(AG)ICCIATIGGIGCIAA

(List 9)

5 SN-1 30mer
CACGAACTGGGGCACGAGACACAGATGATG

SC-3RV 30mer
AAGCAAGTCACGGAGTGTGAATAGTCAGAG

SC-5 30mer
10 ACACGAGACTGTTTGTGTTGAAGACCCCTTG

SC-6 25mer
TGGAATCTCAACAAATATACAGGTG

SN-3RV 30mer
GGGTCATGGCCAACGTGGACGTATAAGCAC

15 SN-4RV 30mer
GATGATCACTGGCGCGGTTTTCTCCTCGAG

Example 10 (Acquisition of Raffinose Synthetase Gene from Japanese Artichoke cDNA)

20 In the same manner as described in Example 5, cDNA was obtained from leaves of Japanese artichoke (*Stachys sieboldii*). Using this cDNA as a template and primers designed from the amino acid sequence of SEQ ID NO:1, i.e., primers having nucleotide sequences shown in list 10 below, a DNA fragment was amplified by PCR under the conditions described in Example 6. The DNA fragment thus amplified by PCR was cloned with a TA cloning kit (Invitrogen), followed by sequence reaction using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit of Perkin-Elmer and nucleotide sequence analysis with a 373S DNA sequencer of ABI. As a result, the nucleotide sequence of SEQ

25 ID:6 was determined.

Based on the nucleotide sequence thus obtained, synthesized DNA primers are prepared, and in the same manner as described in Example 9, the nucleotide sequences in both terminal regions of the gene are analyzed with Marathon Kit of Clontech.

30 (List 10)

1-F primer 35mer
CGATTIAAIGTITGGTGGACIACICAITGGGTIGG

35 4-RV primer 37mer
GGCCAGCIATACICCCITTICCTTAAITGITTIT

2-F primer 44mer
CGAATATIGAIAAITTIGGITGGTGIACITGGGAIGCITTITA

6-RV primer 32mer
40 GGCCACATITTTIACIA(AG)ICCIATIGGIGCIAA

Example 11 (Acquisition of Raffinose Synthetase Gene from Corn cDNA)

45 In the same manner as described in Example 5, cDNA was obtained from leaves of corn (*Zea mays* L.) Pioneer 3358. Using this cDNA as a template and primers designed from the amino acid sequence of SEQ ID NO:1, i.e., primers having nucleotide sequences shown in list 11 below, a DNA fragment was amplified by PCR under the conditions described in Example 6. The DNA fragment thus amplified by PCR was cloned with a TA cloning kit (Invitrogen), followed by sequence reaction using ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit of Perkin-Elmer and nucleotide sequence analysis with a 373S DNA sequencer of ABI. Based on this sequence, primers having nucle-

50 otide sequences shown in list 12 below were synthesized. In the same manner as described in Example 5, mRNA obtained from leaves of corn (*Zea mays* L.) Pioneer 3358 was linked to an adaptor contained in the Marathon Kit of Clontech with ligase. This operation was made according to the protocol attached. Using the adaptor-ligated cDNA thus prepared, polymerase chain reaction was effected in the same manner as described above with the primers shown in list 12 below. As a result, the nucleotide sequence of SEQ ID NO:8 was determined.

55 Based on the nucleotide sequence thus obtained, synthesized DNA primers are prepared, and in the same manner as described in Example 9, the nucleotide sequence in the 5'-terminal region of the gene is analyzed with Marathon Kit of Clontech.

(List 11)

5-F primer 41mer
CGATGGATGGGIAAITTIATICAICCGAITGGGAIATGTT
5 6-RV primer 32mer
GGCCACATITTIACIA(AG)ICCIATIGGIGCIAA

(List 12)

10 M-10 primer 25mer
GACGTCGAGTGGAAGAGCGGCAAGG
M-11 primer 25mer
CACCTACGAGCTCTTCGTCGTGTC

15 Example 12 (Construction of Expression Vectors in Plant for Chimera Gene, 35S-Broad Bean Raffinose Synthetase Gene)

The plasmid pBluescriptKS-RS having the broad bean raffinose synthetase gene obtained in Example 7 was digested with the restriction endonucleases *Bam* HI and *Sac* I. Using Ligation Kit (Takara), the DNA fragment thus digested was cloned in the binary vector pBI121 (Clontech) previously digested with *Bam* HI and *Sac* I. The vector thus obtained was designated pBI121-RS.

For an antisense experiment, plasmid pBI121 (Clontech) previously digested with *Bam* HI and *Sac* I was ligated to linkers shown in list 13 below to give pBI121(-). This pBI121(-) was used to prepare pBI121(-)-RS in the same manner as described for the preparation of pBI121-RS above.

25 A similar vector was prepared with pBI221. The plasmid pBluescriptKS-RS obtained in Example 7 was digested with the restriction endonucleases *Bam* HI and *Sac* I. Using Ligation Kit (Takara), the DNA fragment thus digested was cloned in the vector pBI221 (Clontech) previously digested with *Bam* HI and *Sac* I. The vector thus obtained was designated pBI221-RS.

30 For an antisense experiment, plasmid pBI221 (Clontech) previously digested with *Bam* HI and *Sac* I was ligated to linkers shown in list 13 below to give pBI221(-). This pBI221(-) was used to prepare pBI221(-)-RS in the same manner as described for the preparation of pBI221-RS above.

The construction of these expression vectors is shown in Figures 2 and 3.

(List 13)

35 BamSac-(+) linker 25mer
GATCGAGCTCGTGTCTCGGATCCAGCT
BamSac-(-) linker 17mer
GGATCCGACACGAGCTC

40 Example 13 (Transformation of Mustard with Broad Bean Raffinose Synthetase Gene)

The vectors pBI121-RS and pBI121(-)-RS prepared in Example 12 were used for the transformation of mustard (*Brassica juncea*) by the *Agrobacterium* infection method.

45 *Agrobacterium tumefaciens* (strain C58C1, rifampicin resistant) previously made into a competent state by calcium chloride treatment was transformed independently with two plasmids pBI121-RS and pBI121(-)-RS prepared in Example 12. Selection for transformants was carried out on LB medium containing 50 µg/ml rifampicin and 25 µg/ml kanamycin by utilizing the character of kanamycin resistance conferred by the kanamycin resistance gene (neomycin phosphotransferase, NPTII) of the introduced plasmids.

50 The transformant *Agrobacterium* obtained (*Agrobacterium tumefaciens* strain C58, rifampicin resistant) was cultivated on LB medium containing 50 µg/ml rifampicin and 25 µg/ml kanamycin at 28°C for a whole day and night, and the culture was used for the transformation of mustard by the method described below.

55 The seeds of mustard were aseptically sowed on 1/2 MS medium, 2% sucrose, 0.7% agar. After one week, cotyledons and petioles of sprouting plants were cut out with a scalpel, and transferred to MS medium, 3% sucrose, 0.7% agar, 4.5 µM BA, 0.05 µM 2,4-D, 3.3 µM AgNO₃, followed by precultivation for 1 day. The precultivated cotyledons and petioles were transferred in a 1000-fold dilution of the *Agrobacterium* culture to cause infection for 5 minutes. The infected cotyledons and petioles were transferred again to the same medium as used in the precultivation, and cultivated for 3 to 4 days. The cultivated cotyledons and petioles were transferred to MS medium, 3% sucrose, 4.5 µM BA,

0.05 μ M 2,4-D, 3.3 μ M AgNO₃, 500 mg/l cefotaxim, and sterilized with shaking for 1 day. The sterilized cotyledons and petioles were transferred to MS medium, 3% sucrose, 0.7% agar, 4.5 μ M BA, 0.05 μ M 2,4-D, 3.3 μ M AgNO₃, 100 mg/l cefotaxim, 20 mg/l kanamycin, and cultivated for 3 to 4 weeks. The cotyledons and petioles were transferred to MS medium, 3% sucrose, 0.7% agar, 4.5 μ M BA, 0.05 μ M 2,4-D, 100 mg/l cefotaxim, 20 mg/l kanamycin, and cultivated. The cultivation on this medium was continued with subculturing at intervals of 3 to 4 weeks. When the regeneration of shoots began to occur, these shoots were subcultured on MS medium, 3% sucrose, 0.7% agar, 20 mg/l kanamycin, and cultivated for 3 to 4 weeks. The rooting plants were transferred to vermiculite : peat moss = 1 : 1, and conditioned at 21° to 22°C in a cycle of day/night = 12 hours : 12 hours. With the progress of plant body growth, the plants were suitably grown with cultivation soil. From leaves of the regenerated plants, genomic DNA was extracted according to the method described above, and the gene insertion into the plant genome was confirmed by PCR using the primers shown in list 14 below.

(List 14)

35S 30mer
TTCCAGTATGGACGATTCAAGGCTTGCTTC
NOS 25mer
ATGTATAATTGCGGGACTCTAATCA
RS-F 30mer
AAGAGTGTATCTGAATTTTCACGCGCGGTG
RS-RV 33mer
ACCTTCCCATACACCTTTTGGATGAACCTTCAA

Example 14 (Transformation of Soybean Somatic Embryo with Broad Bean Raffinose Synthetase Gene)

Cultured cells of soybean "Fayette" somatic embryos (400 to 500 mg FW) were arranged in one layer within a circle having a diameter of 20 mm on the central part of a 6 cm agar plate. Two plasmids pBI221-RS and pBI221(-)-RS having chimera genes prepared from the broad bean raffinose synthetase gene and 35S promoter in Example 12 were introduced into the soybean somatic embryos according to the disclosure of the Japanese Patent Application No. 3-291501/1991. That is, these plasmids were mixed with the β -glucuronidase (GUS)/hygromycin-resistant gene (HPT) coexpression vector pSUM-GH:NotI for selection described in Soshiki Baiyo, 20, 323-327 (1994). These mixed plasmids were used for the gene introduction into the soybean somatic embryos with a particle gun (800 mg/coating gold particles 200 μ g/shot; projectile stopper-sample distance, 100 mm). After the introduction, gyratory cultures were grown in the MS modified growth liquid medium (Sigma) containing 25 to 50 μ g/ml hygromycin under illumination at 25°C for 16 hours, and transformed somatic embryos were selected.

For the hygromycin-resistant soybean somatic embryos having yellowish green color and growth ability, which were selected after about 3 months, polymerization chain reaction is effected with primers shown in list 14 above to determine whether the broad bean raffinose synthetase gene region is amplified or not. This confirms that the broad bean raffinose synthetase gene is inserted into the soybean genome.

Furthermore, the somatic embryos obtained are used for the regeneration of plants to give transformant soybean with the broad bean raffinose synthetase gene.

Medium Composition

LB and MS media used in the above Examples have the following respective compositions.

(LB medium)	
Bacto-tryptone	10 g
Bacto-yeast extract	5 g
NaCl	10 g / 1 liter H ₂ O (pH 7.0)

(MS medium)	
KNO ₃	2022 mg/l
NH ₄ NO ₃	1650 mg/l
NH ₄ Cl	2140 mg/l
KH ₂ PO ₄	170 mg/l
MgSO ₄ · 7H ₂ O	370 mg/l
CaCl ₂ · 2H ₂ O	440 mg/l
MnSO ₄ · 4H ₂ O	22.3 mg/l
ZnSO ₄ · 7H ₂ O	8.6 mg/l
CuSO ₄ · 5H ₂ O	0.025 mg/l
KI	0.83 mg/l
CoCl ₂ · 6H ₂ O	0.025 mg/l
H ₃ BO ₃	6.2 mg/l
NaMoO ₄ · 2H ₂ O	0.25 mg/l
FeSO ₄ · 7H ₂ O	27.8 mg/l
Na ₂ EDTA	37.3 mg/l
Nicotinic acid	0.5 mg/l
Thiamine HCl	1 mg/l
Pyridoxine HCl	0.5 mg/l
Inositol	100 mg/l
Glycine	2 mg/l

Brief Description of the Sequences

1. SEQ ID NO:1:

The sequence of SEQ ID NO:1 shows an amino acid sequence of a raffinose synthetase protein encoded in the raffinose synthetase gene obtained from broad bean.

2. SEQ ID NO:2:

The sequence of SEQ ID NO:2 shows a cDNA nucleotide sequence of the raffinose synthetase gene obtained from broad bean.

3. SEQ ID NO:3:

The sequence of SEQ ID NO:3 shows an amino acid sequence of a raffinose synthetase protein encoded in the raffinose synthetase gene obtained from soybean.

4. SEQ ID NO:4:

The sequence of SEQ ID NO:4 shows a cDNA nucleotide sequence of the raffinose synthetase gene obtained from soybean.

5. SEQ ID NO:5:

The sequence of SEQ ID NO:5 shows an amino acid sequence of a raffinose synthetase protein encoded in the raffinose synthetase gene obtained from Japanese artichoke.

6. SEQ ID NO:6:

The sequence of SEQ ID NO:6 shows a cDNA nucleotide sequence of the raffinose synthetase gene obtained from Japanese artichoke.

7. SEQ ID NO:7:

The sequence of SEQ ID NO:7 shows an amino acid sequence of a raffinose synthetase protein encoded in the raffinose synthetase gene obtained from corn.

8. SEQ ID NO:8:

The sequence of SEQ ID NO:8 shows a cDNA nucleotide sequence of the raffinose synthetase gene obtained from corn.

9. List 1:

The nucleotide sequences shown in list 1 are of the typical primers used in the amplification of a cDNA fragment of a raffinose synthetase gene. All of these sequences are based on the nucleotide sequence in the non-coding region of the gene. Primer 1 is a sense primer corresponding to the 5'-terminus of a cDNA fragment of the broad bean-derived raffinose synthetase gene. Primers 2 and 3 are antisense primers corresponding to the 3'-terminus of the cDNA fragment of the broad bean-derived raffinose synthetase gene. Primer 4 is a sense primer corresponding to the 5'-terminus of a cDNA fragment of the soybean-derived raffinose synthetase gene. Primers 5 and 6 are antisense primers corresponding to the 3'-terminus of the cDNA fragment of the soybean-derived raffinose synthetase gene. Depending upon the purpose, recognition sequences for suitable restriction endonucleases can be added to the 5'-termini of these nucleotide sequences in an appropriate manner.

10. List 2:

The nucleotide sequences shown in list 2 are of the typical primers used in the amplification of an open reading frame coding for the amino acid sequence of a raffinose synthetase protein in the cDNA sequence of a raffinose synthetase gene. Primers 1 and 2 are sense primers corresponding to the N-terminus of the broad bean-derived raffinose synthetase protein. Primers 3 and 4 are antisense primers corresponding to the C-terminus of the broad bean-derived raffinose synthetase protein. Primers 5 and 6 are sense primers corresponding to the N-terminus of the soybean-derived raffinose synthetase protein. Primers 7 and 8 are antisense primers corresponding to the C-terminus of the soybean-derived raffinose synthetase protein. Depending upon the purpose, recognition sequences for suitable restriction endonucleases can be added to the 5'-termini of these sequences in an appropriate manner.

11. List 3:

The amino acid sequences shown in list 3 are partial amino acid sequences of a raffinose synthetase protein.

#1 is equivalent to the partial amino acid sequence extending from amino acid 110 to amino acid 129 in the amino acid sequence of SEQ ID NO:1.

#2 is equivalent to the partial amino acid sequence extending from amino acid 234 to amino acid 247 in the amino acid sequence of SEQ ID NO:1.

#3 is equivalent to the partial amino acid sequence extending from amino acid 265 to amino acid 279 in the amino acid sequence of SEQ ID NO:1.

#4 is equivalent to the partial amino acid sequence extending from amino acid 296 to amino acid 312 in the amino acid sequence of SEQ ID NO:1.

#5 is equivalent to the partial amino acid sequence extending from amino acid 346 to amino acid 361 in the amino acid sequence of SEQ ID NO:1.

#6 is equivalent to the partial amino acid sequence extending from amino acid 383 to amino acid 402 in the amino

acid sequence of SEQ ID NO:1.

#7 is equivalent to the partial amino acid sequence extending from amino acid 411 to amino acid 433 in the amino acid sequence of SEQ ID NO:1.

#8 is equivalent to the partial amino acid sequence extending from amino acid 440 to amino acid 453 in the amino acid sequence of SEQ ID NO:1.

#9 is equivalent to the partial amino acid sequence extending from amino acid 457 to amino acid 468 in the amino acid sequence of SEQ ID NO:1.

#10 is equivalent to the partial amino acid sequence extending from amino acid 471 to amino acid 516 in the amino acid sequence of SEQ ID NO:1.

#11 is equivalent to the partial amino acid sequence extending from amino acid 517 to amino acid 559 in the amino acid sequence of SEQ ID NO:1.

#12 is equivalent to the partial amino acid sequence extending from amino acid 574 to amino acid 582 in the amino acid sequence of SEQ ID NO:1.

#13 is equivalent to the partial amino acid sequence extending from amino acid 586 to amino acid 609 in the amino acid sequence of SEQ ID NO:1.

#14 is equivalent to the partial amino acid sequence extending from amino acid 615 to amino acid 627 in the amino acid sequence of SEQ ID NO:1.

#15 is equivalent to the partial amino acid sequence extending from amino acid 716 to amino acid 724 in the amino acid sequence of SEQ ID NO:1.

12. List 4:

The nucleotide sequences shown in list 4 are of the typical primers synthesized on some of the amino acid sequences shown in list 3. The symbol "F" as used after the primer number means that the primer referred to by this symbol has a sense sequence. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence. Primer 1 corresponds to the partial amino acid sequence extending from amino acid 119 to amino acid 129 in the amino acid sequence of SEQ ID NO:1. Primer 2 corresponds to the partial amino acid sequence extending from amino acid 234 to amino acid 247 in the amino acid sequence of SEQ ID NO:1. Primer 3 corresponds to the partial amino acid sequence extending from amino acid 265 to amino acid 279 in the amino acid sequence of SEQ ID NO:1. Primer 4 corresponds to the partial amino acid sequence extending from amino acid 458 to amino acid 468 in the amino acid sequence of SEQ ID NO:1. Primer 5 corresponds to the partial amino acid sequence extending from amino acid 522 to amino acid 534 in the amino acid sequence of SEQ ID NO:1. Primer 6 corresponds to the partial amino acid sequence extending from amino acid 716 to amino acid 724 in the amino acid sequence of SEQ ID NO:1.

13. List 5:

The nucleotide sequences shown in list 5 are of the typical primers synthesized on the partial amino acid sequences of the purified broad bean raffinose synthetase protein. The bases shown in parentheses mean that a mixture of those bases was used in the synthesis. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

14. List 6:

The nucleotide sequences shown in list 6 are of the typical primers used in the analysis of both terminal regions of a cDNA nucleotide sequence of the broad bean raffinose synthetase gene by the RACE method. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

15. List 7:

The nucleotide sequences shown in list 7 are of the typical primers used in the cloning of the broad bean raffinose synthetase gene. RS-N corresponds to the N-terminus of the open reading frame and contains two recognition sites for the restriction endonucleases *Bam* HI and *Nco* I on the 5'-terminal side. RS-C is an antisense primer corresponding to the C-terminus of the open reading frame and contains a recognition site for the restriction endonuclease *Xba* I on the 5'-terminal side.

16. List 8:

The nucleotide sequences shown in list 8 are of the typical primers used in the cloning of a soybean raffinose synthetase gene fragment. The base represented by the symbol "I" was inosine used in the synthesis. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

17. List 9:

The nucleotide sequences shown in list 9 are of the typical primers used in the analysis of the cDNA nucleotide sequence of a soybean raffinose synthetase gene fragment. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

The analysis of nucleotide sequences was carried out by polymerase chain reaction using SN-1 and SC-3RV. SC-5 and SC-6 were used in the analysis of a nucleotide sequence in the 3'-terminal region, and SN-3RV and SN-4RV were used in the analysis of a nucleotide sequence in the 5'-terminal region.

18. List 10:

The nucleotide sequences shown in list 10 are of the typical primers used in the analysis of the cDNA nucleotide sequence of a Japanese artichoke raffinose synthetase gene fragment. The base represented by the symbol "I" was inosine used in the synthesis. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

19. List 11:

The nucleotide sequences shown in list 11 are of the typical primers used in the analysis of the cDNA nucleotide sequence of a corn raffinose synthetase gene fragment. The base represented by the symbol "I" was inosine used in the synthesis. The symbol "RV" as used after the primer number means that the primer referred to by this symbol has an antisense sequence.

20. List 12:

The nucleotide sequences shown in list 12 are of the typical primers used in the analysis of the cDNA nucleotide sequence of a corn raffinose synthetase gene fragment. M-10 and M-11 were used in the analysis of a nucleotide sequence in the 3'-terminal region.

21. List 13:

The nucleotide sequences shown in list 13 are of the typical adopters used in the construction of vectors for anti-sense experiments. These synthetic DNA fragments takes a double-stranded form when mixed together because they are complementary strands. This double-stranded DNA fragment has cohesive ends of cleavage sites for the restriction endonucleases *Bam* HI and *Sac* I on both termini, and contains the restriction sites for the restriction endonucleases *Bam* HI and *Sac* I in the double-stranded region.

22. List 14:

The nucleotide sequences shown in list 14 are of the typical primers used in the PCR experiment to confirm the gene introduction into the genome of a recombinant plant. 35S is a primer toward the downstream region at the 35S promoter site, and NOS is a primer toward the upstream region at the NOS terminator site. RS-F is a sense primer of the broad bean raffinose synthetase gene, and RS-RV is an antisense primer of the broad bean raffinose synthetase gene.

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Sumitomo Chemical Co., Ltd.
- (B) STREET: 5-33, Kitahama 4-chome, Chuo-ku
- (C) CITY: Osaka-shi, Osaka-fu
- (E) COUNTRY: Japan
- (F) POSTAL CODE (ZIP): none

(ii) TITLE OF INVENTION: Raffinose synthetase genes and the use thereof

(iii) NUMBER OF SEQUENCES: 8

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PS-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 97 12 2417.5
- (B) FILING DATE: 18-DEC-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 338673/1996
- (B) FILING DATE: 18-DEC-1996

(1) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: broad bean (Vicia faba)
- (B) STRAIN: Nintoku Issun
- (F) TISSUE TYPE: seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Pro	Pro	Ser	Ile	Thr	Lys	Thr	Ala	Thr	Leu	Gln	Asp	Val	Ile	1	5	10	15
Ser	Thr	Ile	Asp	Ile	Gly	Asn	Gly	Asn	Ser	Pro	Leu	Phe	Ser	Ile	Thr	20	25	30	
Leu	Asp	Gln	Ser	Arg	Asp	Phe	Leu	Ala	Asn	Gly	His	Pro	Phe	Leu	Thr	35	40	45	
Gln	Val	Pro	Pro	Asn	Ile	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ser	Ser	50	55	60	
Phe	Leu	Asn	Leu	Lys	Ser	Asn	Lys	Asp	Thr	Ile	Pro	Asn	Asn	Asn	Asn	65	70	75	80

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	Thr	Met	Leu	Leu	Gln	Gln	Gly	Cys	Phe	Val	Gly	Phe	Asn	Ser	Thr	Glu
					85					90					95	
5	Pro	Lys	Ser	His	Val	Val	Pro	Leu	Gly	Lys	Leu	Lys	Gly	Ile	Lys	
				100				105					110			
	Phe	Met	Ser	Ile	Phe	Arg	Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val
			115					120					125			
	Gly	Thr	Asn	Gly	Gln	Glu	Leu	Gln	His	Glu	Thr	Gln	Met	Leu	Ile	Leu
			130					135				140				
10	Asp	Lys	Asn	Asp	Ser	Leu	Gly	Arg	Pro	Tyr	Val	Leu	Leu	Leu	Pro	Ile
			145			150					155					160
	Leu	Glu	Asn	Thr	Phe	Arg	Thr	Ser	Leu	Gln	Pro	Gly	Leu	Asn	Asp	His
				165						170					175	
	Ile	Gly	Met	Ser	Val	Glu	Ser	Gly	Ser	Thr	His	Val	Thr	Gly	Ser	Ser
				180					185					190		
15	Phe	Lys	Ala	Cys	Leu	Tyr	Ile	His	Leu	Ser	Asn	Asp	Pro	Tyr	Ser	Ile
			195					200					205			
	Leu	Lys	Glu	Ala	Val	Lys	Val	Ile	Gln	Thr	Gln	Leu	Gly	Thr	Phe	Lys
			210					215				220				
	Thr	Leu	Glu	Glu	Lys	Thr	Ala	Pro	Ser	Ile	Ile	Asp	Lys	Phe	Gly	Trp
			225			230					235					240
20	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Lys	Val	His	Pro	Lys	Gly	Val	Trp
				245						250					255	
	Glu	Gly	Val	Lys	Ser	Leu	Thr	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Phe	Val
				260					265					270		
	Ile	Ile	Asp	Asp	Gly	Trp	Gln	Ser	Ile	Cys	His	Asp	Asp	Asp	Asp	Glu
			275				280						285			
25	Asp	Asp	Ser	Gly	Met	Asn	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys
			290				295					300				
	Arg	Leu	Val	Lys	Tyr	Glu	Glu	Asn	Ser	Lys	Phe	Arg	Glu	Tyr	Glu	Asn
					310						315					
30	Pro	Glu	Asn	Gly	Gly	Lys	Lys	Gly	Leu	Gly	Gly	Phe	Val	Arg	Asp	Leu
				325					330						335	
	Lys	Glu	Glu	Phe	Gly	Ser	Val	Glu	Ser	Val	Tyr	Val	Trp	His	Ala	Leu
				340					345					350		
	Cys	Gly	Tyr	Trp	Gly	Gly	Val	Arg	Pro	Gly	Val	His	Gly	Met	Pro	Lys
			355				360						365			
35	Ala	Arg	Val	Val	Val	Pro	Lys	Val	Ser	Gln	Gly	Leu	Lys	Met	Thr	Met
			370				375					380				
	Glu	Asp	Leu	Ala	Val	Asp	Lys	Ile	Val	Glu	Asn	Gly	Val	Gly	Leu	Val
					390					395						400
	Pro	Pro	Asp	Phe	Ala	His	Glu	Met	Phe	Asp	Gly	Leu	His	Ser	His	Leu
				405						410					415	
40	Glu	Ser	Ala	Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	Leu
				420					425					430		
	Glu	Leu	Leu	Ser	Glu	Glu	Tyr	Gly	Gly	Arg	Val	Glu	Leu	Ala	Arg	Ala
			435				440						445			
	Tyr	Tyr	Lys	Ala	Leu	Thr	Ser	Ser	Val	Lys	Lys	His	Phe	Lys	Gly	Asn
			450				455					460				
45	Gly	Val	Ile	Ala	Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Phe	Leu	Leu	Gly
					470					475						480
	Thr	Glu	Ala	Ile	Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Ser
				485						490					495	
	Asp	Pro	Ser	Gly	Asp	Pro	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His
				500				505					510			
50	Met	Val	His	Cys	Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	Gln
			515					520					525			
	Pro	Asp	Trp	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His
				530			535					540				

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Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys
 545 550 555 560
 Val Gly Asn His Asn Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp
 565 570 575
 Gly Ser Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys
 580 585 590
 Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp
 595 600 605
 Asn Leu Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly
 610 615 620
 Gly Gly Trp Cys Pro Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe
 625 630 635 640
 Ser Arg Ala Val Thr Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys
 645 650 655
 Asn Gly Lys Thr Pro Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val
 660 665 670
 Tyr Phe Phe Lys Glu Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg
 675 680 685
 Leu Lys Val Ser Leu Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser
 690 695 700
 Pro Val Lys Val Phe Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly
 705 710 715 720
 Leu Val Asn Met Leu Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe
 725 730 735
 Asp Asp Asn Ala Ser Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu
 740 745 750
 Met Ser Val Phe Ala Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly
 755 760 765
 Val Lys Val Lys Phe Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile
 770 775 780
 Leu Trp Pro Ser Ser Ser Thr Leu Ser Leu Val Gln Phe Leu Phe Stop
 785 790 795 800

(1) INFORMATION FOR SEQ ID NO:2:

(i). SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 101..2500
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTTCAAG CATAGCCAAG TTAACCACCT TAGAAACATT CCTACAAGCT ACTTATCCCT 60
 GTCAATAAGC TACTAAGCTA CCAGAGTCTC ATCAATCACC ATG GCA CCA CCA AGC 115
 Met Ala Pro Pro Ser 5
 ATA ACC AAA ACT GCA ACC CTC CAA GAC GTA ATA AGC ACC ATC GAT ATT 163
 Ile Thr Lys Thr Ala Thr Leu Gln Asp Val Ile Ser Thr Ile Asp Ile
 10 15 20

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	GGT	AAT	GGT	AAC	TCA	CCC	TTA	TTC	TCC	ATA	ACC	TTA	GAC	CAA	TCA	CGT	211
	Gly	Asn	Gly	Asn	Ser	Pro	Leu	Phe	Ser	Ile	Thr	Leu	Asp	Gln	Ser	Arg	
				25					30					35			
5	GAC	TTC	CTT	GCA	AAT	GGC	CAC	CCT	TTC	CTC	ACC	CAA	GTC	CCA	CCT	AAC	259
	Asp	Phe	Leu	Ala	Asn	Gly	His	Pro	Phe	Leu	Thr	Gln	Val	Pro	Pro	Asn	
			40					45					50				
	ATA	ACA	ACA	ACA	ACA	ACC	ACT	GCT	TCC	TCT	TTT	CTC	AAT	CTC	AAA		307
	Ile	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ser	Ser	Phe	Leu	Asn	Leu	Lys		
			55				60					65					
10	TCC	AAC	AAA	GAT	ACC	ATT	CCC	AAC	AAC	AAC	AAC	ACC	ATG	TTG	TTG	CAA	355
	Ser	Asn	Lys	Asp	Thr	Ile	Pro	Asn	Asn	Asn	Asn	Thr	Met	Leu	Leu	Gln	
			70			75					80					85	
	CAA	GGT	TGT	TTC	GTT	GGT	TTC	AAC	TCC	ACC	GAA	CCC	AAA	AGC	CAC	CAC	403
	Gln	Gly	Cys	Phe	Val	Gly	Phe	Asn	Ser	Thr	Glu	Pro	Lys	Ser	His	His	
				90						95				100			
15	GTA	GTT	CCA	CTC	GGC	AAA	CTA	AAA	GGA	ATC	AAA	TTC	ATG	AGC	ATA	TTC	451
	Val	Val	Pro	Leu	Gly	Lys	Leu	Lys	Gly	Ile	Lys	Phe	Met	Ser	Ile	Phe	
				105					110					115			
	CGG	TTC	AAA	GTT	TGG	TGG	ACA	ACT	CAC	TGG	GTC	GGA	ACA	AAT	GGA	CAG	499
	Arg	Phe	Lys	Val	Trp	Trp	Thr	His	Trp	Val	Gly	Thr	Asn	Gly	Gln		
20				120				125					130				
	GAA	CTA	CAA	CAC	GAA	ACA	CAA	ATG	TTA	ATC	CTG	GAC	AAA	AAC	GAC	TCC	547
	Glu	Leu	Gln	His	Glu	Thr	Gln	Met	Leu	Ile	Leu	Asp	Lys	Asn	Asp	Ser	
				135			140					145					
	CTC	GGA	CGA	CCC	TAT	GTC	TTA	CTC	CTC	CCA	ATC	CTA	GAA	AAC	ACC	TTC	595
	Leu	Gly	Arg	Pro	Tyr	Val	Leu	Leu	Leu	Pro	Ile	Leu	Glu	Asn	Thr	Phe	
25				150		155					160				165		
	CGA	ACC	TCA	CTC	CAA	CCC	GGT	CTC	AAC	GAT	CAC	ATA	GGC	ATG	TCC	GTC	643
	Arg	Thr	Ser	Leu	Gln	Pro	Gly	Leu	Asn	Asp	His	Ile	Gly	Met	Ser	Val	
				170						175					180		
	GAA	AGC	GGT	TCA	ACA	CAT	GTC	ACC	GGG	TCA	AGC	TTC	AAA	GCA	TGT	CTT	691
	Glu	Ser	Gly	Ser	Thr	His	Val	Thr	Ser	Ser	Phe	Lys	Ala	Cys	Leu		
30				185					190					195			
	TAC	ATC	CAT	CTC	AGT	AAC	GAC	CCA	TAC	AGT	ATA	CTA	AAA	GAA	GCA	GTT	739
	Tyr	Ile	His	Leu	Ser	Asn	Asp	Pro	Tyr	Ser	Ile	Leu	Lys	Glu	Ala	Val	
				200				205					210				
	AAA	GTA	ATC	CAA	ACT	CAG	TTA	GGA	ACA	TTC	AAG	ACT	CTT	GAA	GAA	AAA	787
	Lys	Val	Ile	Gln	Thr	Gln	Leu	Gly	Thr	Phe	Lys	Thr	Leu	Glu	Glu	Lys	
35				215			220					225					
	ACA	GCA	CCT	AGT	ATT	ATA	GAC	AAA	TTC	GGT	TGG	TGC	ACG	TGG	GAT	GCT	835
	Thr	Ala	Pro	Ser	Ile	Ile	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	
				230		235					240				245		
40	TTT	TAC	TTG	AAG	GTT	CAT	CCA	AAA	GGT	GTA	TGG	GAA	GGT	GTA	AAG	TCT	883
	Phe	Tyr	Leu	Lys	Val	His	Pro	Lys	Gly	Val	Trp	Glu	Gly	Val	Lys	Ser	
				250						255				260			
	CTC	ACA	GAT	GGT	GGT	TGT	CCT	CCC	GGT	TTC	GTC	ATA	ATC	GAC	GAC	GGT	931
	Leu	Thr	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Phe	Val	Ile	Ile	Asp	Asp	Gly	
				265					270					275			
45	TGG	CAA	TCC	ATT	TGT	CAT	GAC	GAT	GAC	GAT	GAA	GAT	GAT	TCA	GGA	ATG	979
	Trp	Gln	Ser	Ile	Cys	His	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Ser	Gly	Met	
				280				285						290			
	AAC	CGA	ACC	TCA	GCC	GGG	GAA	CAA	ATG	CCA	TGC	AGA	CTT	GTA	AAA	TAC	1027
	Asn	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Val	Lys	Tyr	
				295			300					305					
50	GAA	GAG	AAT	TCT	AAG	TTT	AGA	GAA	TAT	GAG	AAT	CCT	GAA	AAT	GGA	GGG	1075
	Glu	Glu	Asn	Ser	Lys		Arg	Glu	Tyr	Glu	Asn	Pro	Glu	Asn	Gly	Gly	
						315					320					325	
	310																

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	AAG AAA GGT TTG GGT GGT TTT GTG AGG GAT TTG AAG GAA GAG TTT GGG	1123
	Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu Lys Glu Glu Phe Gly	
5	330 335 340	
	AGT GTG GAG AGT GTT TAT GTT TGG CAT GCG CTT TGT GGG TAT TGG GGC	1171
	Ser Val Glu Ser Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly	
	345 350 355	
	GGG GTT AGG CCT GGA GTG CAT GGG ATG CCG AAA GCT AGG GTT GTT GTT	1219
	Gly Val Arg Pro Gly Val His Gly Met Pro Lys Ala Arg Val Val Val	
10	360 365 370	
	CCG AAG GTG TCT CAG GGG TTG AAG ATG ACG ATG GAG GAT TTG GCG GTG	1267
	Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met Glu Asp Leu Ala Val	
	375 380 385	
	GAT AAG ATT GTT GAG AAC GGT GTG GGG CTA GTG CCG CCA GAT TTT GCA	1315
	Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val Pro Pro Asp Phe Ala	
15	390 395 400 405	
	CAT GAG ATG TTT GAT GGG CTT CAC TCT CAT TTG GAG TCG GCG GGA ATT	1363
	His Glu Met Phe Asp Gly Leu His Ser His Leu Glu Ser Ala Gly Ile	
	410 415 420	
	GAC GGT GTT AAA GTT GAT GTT ATC CAT CTG CTT GAG TTA CTA TCA GAG	1411
	Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Leu Ser Glu	
20	425 430 435	
	GAA TAT GGT GGA CGA GTT GAG CTA GCA AGA GCT TAT TAC AAA GCA CTA	1459
	Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu	
	440 445 450	
	ACC TCA TCA GTG AAG AAA CAT TTC AAA GGC AAT GGT GTA ATT GCT AGC	1507
25	Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala Ser	
	455 460 465	
	ATG GAG CAT TGC AAC GAC TTC TTT CTC CTC GGC ACC GAA GCC ATA TCC	1555
	Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser	
	470 475 480 485	
	CTC GGC CGC GTC GGA GAT GAT TTT TGG TGC TCT GAT CCA TCT GGT GAT	1603
30	Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser Asp Pro Ser Gly Asp	
	490 495 500	
	CCA AAT GGT ACA TAT TGG CTC CAA GGT TGT CAC ATG GTA CAT TGT GCC	1651
	Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys Ala	
	505 510 515	
	TAC AAC AGT TTA TGG ATG GGA AAT TTC ATT CAG CCA GAT TGG GAC ATG	1699
35	Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp Met	
	520 525 530	
	TTT CAG TCC ACT CAT CCT TGT GCT GAA TTT CAT GCC GCC TCA CGA GCC	1747
	Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg Ala	
	535 540 545	
	ATA TCC GGC GGA CCA ATT TAT GTT AGT GAT TGT GTT GGT AAT CAC AAT	1795
40	Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys Val Gly Asn His Asn	
	550 555 560 565	
	TTC AAG TTG CTC AAA TCT CTT GTT TTG CCC GAT GGT TCT ATC TTG CGT	1843
	Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp Gly Ser Ile Leu Arg	
	570 575 580	
	TGT CAA CAT TAC GCA CTC CCT ACA AGA GAT TGC TTG TTT GAA GAC CCT	1891
45	Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro	
	585 590 595	
	TTG CAT AAT GGC AAA ACA ATG CTG AAA ATT TGG AAT CTC AAC AAA TAT	1939
	Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Tyr	
	600 605 610	
50	ACA GGT GTT TTG GGT CTT TTC AAC TGC CAA GGT GGT GGG TGG TGT CCT	1987
	Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro	
	615 620 625	

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GAG GCA CGG CGA AAC AAG AGT GTA TCT GAA TTT TCA CGC GCG GTG ACA 2035
 Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe Ser Arg Ala Val Thr
 630 635 640 645
 5 TGT TAT GCA AGT CCC GAA GAC ATT GAA TGG TGC AAT GGG AAA ACT CCA 2083
 Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys Asn Gly Lys Thr Pro
 650 655 660
 ATG AGC ACC AAA GGT GTG GAT TTT TTT GCT GTG TAT TTT TTC AAG GAG 2131
 Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val Tyr Phe Phe Lys Glu
 665 670 675
 10 AAG AAA TTG AGG CTC ATG AAG TGT TCT GAT AGA TTG AAA GTT TCG CTT 2179
 Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg Leu Lys Val Ser Leu
 680 685 690
 GAG CCA TTT AGT TTT GAG CTA ATG ACA GTG TCT CCA GTG AAA GTG TTT 2227
 Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser Pro Val Lys Val Phe
 695 700 705
 15 TCG AAA AGG TTT ATA CAG TTT GCA CCG ATT GGG TTA GTG AAC ATG CTG 2275
 Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu
 710 715 720 725
 AAC TCT GGT GGT GCG ATT CAG TCT CTG GAG TTT GAT GAT AAT GCA AGT 2323
 Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe Asp Asp Asn Ala Ser
 730 735 740
 20 TTG GTC AAG ATT GGG GTG AGA GGT TGC GGG GAG ATG AGC GTG TTT GCG 2371
 Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Ser Val Phe Ala
 745 750 755
 TCT GAG AAA CCG GTT TGC TGC AAA ATT GAT GGG GTT AAG GTG AAA TTT 2419
 Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly Val Lys Val Lys Phe
 760 765 770
 25 CTT TAT GAG GAC AAA ATG GCA AGA GTT CAA ATT CTG TGG CCT AGT TCT 2467
 Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile Leu Trp Pro Ser Ser
 775 780 785
 TCA ACA TTG TCT TTG GTC CAG TTT TTA TTT TGA TCCCTAGGAA TCCTATGCAC 2520
 Ser Thr Leu Ser Leu Val Gln Phe Leu Phe Stop
 790 795 800
 30 GTGTCTCTGT TTACAAGTAC TTTATATAAG TATAATATGT ATCTATTTCC ATTTTAACT 2580
 GTCTTTATGC AATTAGGTGG TCAATTAGTT ATTTGTTTGT GAAGTAACTA ACTTGCTTGT 2640
 GTTGTAAGCT TATAATATAT GGTCAAGTTC CTCACTTGTA TATACCTGTT GTATGTATAA 2700
 ATTTTACTAT ATATGACTAA CATCATTATC TTGTGAGCAA AAAAAA 2746

(1) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: soybean (Glycine max)
- (B) STRAIN: Williams 82
- (F) TISSUE TYPE: seeds and leaves

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Pro Ser Ile Ser Lys Thr Val Glu Leu Asn Ser Phe Gly Leu
 5 10 15
 Val Asn Gly Asn Leu Pro Leu Ser Ile Thr Leu Glu Gly Ser Asn Phe
 20 25 30

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Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile Ile
 35 40 45
 Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu Asp
 5 50 55 60
 Asp Asp Val Val Gly Cys Phe Val Gly Phe His Ala Asp Glu Pro Arg
 65 70 75 80
 Ser Arg His Val Ala Ser Leu Gly Lys Leu Arg Gly Ile Lys Phe Met
 85 90 95
 Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Ser
 10 100 105 110
 Asn Gly His Glu Leu Glu His Glu Thr Gln Met Met Leu Leu Asp Lys
 115 120 125
 Asn Asp Gln Leu Gly Arg Pro Phe Val Leu Ile Leu Pro Ile Leu Gln
 130 135 140
 Ala Ser Phe Arg Ala Ser Leu Gln Pro Gly Leu Asp Asp Tyr Val Asp
 145 150 155 160
 Val Cys Met Glu Ser Gly Ser Thr Arg Val Cys Gly Ser Ser Phe Gly
 165 170 175
 Ser Cys Leu Tyr Val His Val Gly His Asp Pro Tyr Gln Leu Leu Arg
 180 185 190
 Glu Ala Thr Lys Val Val Arg Met His Leu Gly Thr Phe Lys Leu Leu
 195 200 205
 Glu Glu Lys Thr Ala Pro Val Ile Ile Asp Lys Phe Gly Trp Cys Thr
 210 215 220
 Trp Asp Ala Phe Tyr Leu Lys Val His Pro Ser Gly Val Trp Glu Gly
 225 230 235 240
 Val Lys Gly Leu Val Glu Gly Gly Cys Pro Pro Gly Met Val Leu Ile
 245 250 255
 Asp Asp Gly Trp Gln Ala Ile Cys His Asp Glu Asp Pro Ile Thr Asp
 260 265 270
 Gln Glu Gly Met Lys Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg
 275 280 285
 Leu Val Lys Leu Glu Glu Asn Tyr Lys Phe Arg Gln Tyr Cys Ser Gly
 290 295 300
 Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys Glu
 305 310 315 320
 Gln Phe Arg Ser Val Glu Gln Val Tyr Val Trp His Ala Leu Cys Gly
 325 330 335
 Tyr Trp Gly Gly Val Arg Pro Lys Val Pro Gly Met Pro Gln Ala Lys
 340 345 350
 Val Val Thr Pro Lys Leu Ser Asn Gly Leu Lys Leu Thr Met Lys Asp
 355 360 365
 Leu Ala Val Asp Lys Ile Val Ser Asn Gly Val Gly Leu Val Pro Pro
 370 375 380
 His Leu Ala His Leu Leu Tyr Glu Gly Leu His Ser Arg Leu Glu Ser
 385 390 395 400
 Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met
 405 410 415
 Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Lys Ala Tyr Tyr
 420 425 430
 Lys Ala Leu Thr Ala Ser Val Lys Lys His Phe Lys Gly Asn Gly Val
 435 440 445
 Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu
 450 455 460
 Ala Ile Ala Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro
 465 470 475 480
 Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val
 485 490 495

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His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp
500 505 510
Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala
515 520 525
Ser Arg Ala Ile Ser Gly Gly Pro Val Tyr Val Ser Asp Cys Val Gly
530 535 540
Lys His Asn Phe Lys Leu Leu Lys Ser Leu Ala Leu Pro Asp Gly Thr
545 550 555 560
Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe
565 570 575
Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu
580 585 590
Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly
595 600 605
Trp Cys Pro Val Thr Arg Arg Asn Lys Ser Ala Ser Glu Phe Ser Gln
610 615 620
Thr Val Thr Cys Leu Ala Ser Pro Gln Asp Ile Glu Trp Ser Asn Gly
625 630 635 640
Lys Ser Pro Ile Cys Ile Lys Gly Met Asn Val Phe Ala Val Tyr Leu
645 650 655
Phe Lys Asp His Lys Leu Lys Leu Met Lys Ala Ser Glu Lys Leu Glu
660 665 670
Val Ser Leu Glu Pro Phe Thr Phe Glu Leu Leu Thr Val Ser Pro Val
675 680 685
Ile Val Leu Ser Lys Lys Leu Ile Gln Phe Ala Pro Ile Gly Leu Val
690 695 700
Asn Met Leu Asn Thr Gly Gly Ala Ile Gln Ser Met Glu Phe Asp Asn
705 710 715 720
His Ile Asp Val Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Lys
725 730 735
Val Phe Ala Ser Glu Lys Pro Val Ser Cys Lys Leu Asp Gly Val Val
740 745 750
Val Lys Phe Asp Tyr Glu Asp Lys Met Leu Arg Val Gln Val Pro Trp
755 760 765
Pro Ser Ala Ser Lys Leu Ser Met Val Glu Phe Leu Phe Stop
770 775 780

(1) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 62..2407
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCAAACCATTA GCAAACCTAA GCACCAAACC TCTTCTTTTC AAGATCCTTG AATTCAGTCC 60
C ATG GCT CCA AGC ATA AGC AAA ACT GTG GAA CTA AAT TCA TTT GGT 106
Met Ala Pro Ser Ile Ser Lys Thr Val Glu Leu Asn Ser Phe Gly
5 10 15

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	CTT GTC AAC GGT AAT TTG CCT TTG TCC ATA ACC CTA GAA GGA TCA AAT	154
	Leu Val Asn Gly Asn Leu Pro Leu Ser Ile Thr Leu Glu Gly Ser Asn	
	20 25 30	
5	TTC CTC GCC AAC GGC CAC CCT TTT CTC ACG GAA GTT CCC GAA AAC ATA	202
	Phe Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile	
	35 40 45	
	ATA GTC ACC CCT TCA CCC ATC GAC GCC AAG AGT AGT AAG AAC AAC GAG	250
	Ile Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu	
	50 55 60	
10	GAC GAC GAC GTC GTA GGT TGC TTC GTG GGC TTC CAC GCG GAC GAG CCC	298
	Asp Asp Asp Val Val Gly Cys Phe Val Gly Phe His Ala Asp Glu Pro	
	65 70 75	
	AGA AGC CGA CAC GTG GCT TCC CTG GGG AAG CTC AGA GGA ATA AAA TTC	346
	Arg Ser Arg His Val Ala Ser Leu Gly Lys Leu Arg Gly Ile Lys Phe	
	80 85 90 95	
15	ATG AGC ATA TTC CGG TTT AAG GTG TGG TGG ACC ACT CAC TGG GTC GGT	394
	Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly	
	100 105 110	
	AGC AAC GGA CAC GAA CTG GAG CAC GAG ACA CAG ATG ATG CTT CTC GAC	442
	Ser Asn Gly His Glu Leu Glu His Glu Thr Gln Met Met Leu Leu Asp	
	115 120 125	
20	AAA AAC GAC CAG CTC GGA CGC CCC TTT GTG TTG ATT CTC CCG ATC CTC	490
	Lys Asn Asp Gln Leu Gly Arg Pro Phe Val Leu Ile Leu Pro Ile Leu	
	130 135 140	
	CAA GCC TCG TTC CGA GCC TCC CTG CAA CCC GGT TTG GAT GAT TAC GTG	538
	Gln Ala Ser Phe Arg Ala Ser Leu Gln Pro Gly Leu Asp Asp Tyr Val	
	145 150 155	
25	GAC GTT TGC ATG GAG AGC GGG TCG ACA CGT GTC TGT GGC TCC AGC TTC	586
	Asp Val Cys Met Glu Ser Gly Ser Thr Arg Val Cys Gly Ser Ser Phe	
	160 165 170 175	
	GGG AGC TGC TTA TAC GTC CAC GTT GGC CAT GAC CCG TAT CAG TTG CTT	634
	Gly Ser Cys Leu Tyr Val His Val Gly His Asp Pro Tyr Gln Leu Leu	
	180 185 190	
30	AGA GAA GCA ACT AAA GTC GTT AGG ATG CAT TTG GGG ACG TTC AAG CTT	682
	Arg Glu Ala Thr Lys Val Val Arg Met His Leu Gly Thr Phe Lys Leu	
	195 200 205	
	CTC GAG GAG AAA ACC GCG CCA GTG ATC ATA GAC AAG TTT GGT TGG TGT	730
	Leu Glu Glu Lys Thr Ala Pro Val Ile Ile Asp Lys Phe Gly Trp Cys	
	210 215 220	
35	ACA TGG GAC GCG TTT TAC TTG AAG GTG CAT CCC TCA GGT GTG TGG GAA	778
	Thr Trp Asp Ala Phe Tyr Leu Lys Val His Pro Ser Gly Val Trp Glu	
	225 230 235	
40	GGG GTG AAA GGG TTG GTG GAG GGA GGG TGC CCT CCA GGG ATG GTC CTA	826
	Gly Val Lys Gly Leu Val Glu Gly Gly Cys Pro Pro Gly Met Val Leu	
	240 245 250 255	
	ATC GAC GAC GGG TGG CAA GCC ATT TGT CAC GAC GAG GAC CCC ATA ACG	874
	Ile Asp Asp Gly Trp Gln Ala Ile Cys His Asp Glu Asp Pro Ile Thr	
	260 265 270	
45	GAC CAA GAG GGT ATG AAG CGA ACC TCC GCA GGG GAG CAA ATG CCA TGC	922
	Asp Gln Glu Gly Met Lys Arg Thr Ser Ala Gly Glu Gln Met Pro Cys	
	275 280 285	
	AGG TTG GTG AAG TTG GAG GAA AAT TAC AAG TTC AGA CAG TAT TGT AGT	970
	Arg Leu Val Lys Leu Glu Glu Asn Tyr Lys Phe Arg Gln Tyr Cys Ser	
	290 295 300	
50	GGG AAG GAT TCT GAG AAG GGT ATG GGT GCC TTT GTT AGG GAC TTG AAG	1018
	Gly Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys	
	305 310 315	

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	GAA	CAG	TTT	AGG	AGC	GTG	GAG	CAG	GTG	TAT	GTG	TGG	CAC	GCG	CTT	TGT	1066
	Glu	Gln	Phe	Arg	Ser	Val	Glu	Gln	Val	Tyr	Val	Trp	His	Ala	Leu	Cys	
	320					325					330					335	
5	GGG	TAT	TGG	GGT	GGG	GTC	AGA	CCC	AAG	GTT	CCG	GGC	ATG	CCC	CAG	GCT	1114
	Gly	Tyr	Trp	Gly	Gly	Val	Arg	Pro	Lys	Val	Pro	Gly	Met	Pro	Gln	Ala	
					340					345						350	
	AAG	GTT	GTC	ACT	CCG	AAG	CTG	TCC	AAT	GGA	CTA	AAA	TTG	ACA	ATG	AAG	1162
	Lys	Val	Val	Thr	Pro	Lys	Leu	Ser	Asn	Gly	Leu	Lys	Leu	Thr	Met	Lys	
				355					360					365			
10	GAT	TTA	GCG	GTG	GAT	AAG	ATC	GTC	AGT	AAC	GGA	GTT	GGA	CTG	GTG	CCA	1210
	Asp	Leu	Ala	Val	Asp	Lys	Ile	Val	Ser	Asn	Gly	Val	Gly	Leu	Val	Pro	
		370					375						380				
	CCA	CAC	CTG	GCT	CAC	CTT	TTG	TAC	GAG	GGG	CTC	CAC	TCC	CGT	TTG	GAA	1258
	Pro	His	Leu	Ala	His	Leu	Leu	Tyr	Glu	Gly	Leu	His	Ser	Arg	Leu	Glu	
		385					390					395					
15	TCT	GCG	GGT	ATT	GAC	GGT	GTT	AAG	GTT	GAC	GTT	ATA	CAC	TTG	CTC	GAG	1306
	Ser	Ala	Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	Leu	Glu	
	400					405				410						415	
	ATG	CTA	TCC	GAG	GAA	TAC	GGT	GGC	CGT	GTT	GAG	CTA	GCC	AAA	GCT	TAT	1354
	Met	Leu	Ser	Glu	Glu	Tyr	Gly	Gly	Arg	Val	Glu	Leu	Ala	Lys	Ala	Tyr	
				420					425						430		
20	TAC	AAA	GCG	CTC	ACT	GCT	TCG	GTG	AAG	AAG	CAT	TTC	AAA	GGC	AAT	GGG	1402
	Tyr	Lys	Ala	Leu	Thr	Ala	Ser	Val	Lys	Lys	His	Phe	Lys	Gly	Asn	Gly	
				435					440				445				
	GTC	ATT	GCG	AGC	ATG	GAG	CAT	TGT	AAT	GAC	TTC	TTT	CTC	CTT	GGT	ACC	1450
	Val	Ile	Ala	Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Phe	Leu	Leu	Gly	Thr	
25				450				455					460				
	GAA	GCC	ATA	GCC	CTT	GGG	CGC	GTA	GGA	GAT	GAT	TTT	TGG	TGC	ACT	GAT	1498
	Glu	Ala	Ile	Ala	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	
		465				470					475						
	CCC	TCT	GGA	GAT	CCA	AAT	GGC	ACG	TAT	TGG	CTC	CAA	GGG	TGT	CAC	ATG	1546
	Pro	Ser	Gly	Asp	Pro	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His	Met	
30		480				485				490					495		
	GTG	CAC	TGT	GCC	TAC	AAC	AGC	TTG	TGG	ATG	GGG	AAT	TTT	ATT	CAG	CCG	1594
	Val	His	Cys	Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	Gln	Pro	
					500				505						510		
35	GAT	TGG	GAC	ATG	TTC	CAG	TCC	ACT	CAC	CCT	TGT	GCC	GAA	TTC	CAT	GC	1642
	Asp	Trp	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His	Ala	
				515					520					525			
	GCC	TCT	AGG	GCC	ATC	TCT	GGT	GGA	CCA	GTT	TAC	GTT	AGT	GAT	TGT	GTT	1690
	Ala	Ser	Arg	Ala	Ile	Ser	Gly	Gly	Pro	Val	Tyr	Val	Ser	Asp	Cys	Val	
				530				535					540				
40	GGA	AAG	CAC	AAC	TTC	AAG	TTG	CTC	AAG	AGC	CTC	GCT	TTG	CCT	GAT	GGG	1738
	Gly	Lys	His	Asn	Phe	Lys	Leu	Leu	Lys	Ser	Leu	Ala	Leu	Pro	Asp	Gly	
		545					550					555					
	ACG	ATT	TTG	CGT	TGT	CAA	CAC	TAT	GCA	CTC	CCC	ACA	CGA	GAC	TGT	TTG	1786
	Thr	Ile	Leu	Arg	Cys	Gln	His	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys	Leu	
45						560				565			570			575	
	TTT	GAA	GAC	CCC	TTG	CAT	GAT	GGG	AAG	ACA	ATG	CTC	AAA	ATT	TGG	AAT	1834
	Phe	Glu	Asp	Pro	Leu	His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	
					580				585						590		
	CTC	AAC	AAA	TAT	ACA	GGT	GTT	TTG	GGT	CTA	TTT	AAT	TGC	CAA	GGA	GGT	1882
	Leu	Asn	Lys	Tyr	Thr	Gly	Val	Leu	Gly	Leu	Phe	Asn	Cys	Gln	Gly	Gly	
50					595				600					605			
	GGG	TGG	TGT	CCC	GTA	ACT	AGG	AGA	AAC	AAG	AGT	GCC	TCT	GAA	TTT	TCA	1930
	Gly	Trp	Cys	Pro	Val	Thr	Arg	Arg	Asn	Lys	Ser	Ala	Ser	Glu	Phe	Ser	
				610				615						620			

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CAA ACT GTG ACA TGC TTA GCG AGT CCT CAA GAC ATT GAA TGG AGC AAT 1978
 Gln Thr Val Thr Cys Leu Ala Ser Pro Gln Asp Ile Glu Trp Ser Asn
 625 630 635
 GGG AAA AGC CCA ATA TGC ATA AAA GGG ATG AAT GTG TTT GCT GTA TAT 2026
 Gly Lys Ser Pro Ile Cys Ile Lys Gly Met Asn Val Phe Ala Val Tyr
 640 645 650 655
 TTG TTC AAG GAC CAC AAA CTA AAG CTC ATG AAG GCA TCA GAG AAA TTG 2074
 Leu Phe Lys Asp His Lys Leu Lys Leu Met Lys Ala Ser Glu Lys Leu
 660 665 670
 GAA GTT TCA CTT GAG CCA TTT ACT TTT GAG CTA TTG ACA GTG TCT CCA 2122
 Glu Val Ser Leu Glu Pro Phe Thr Phe Glu Leu Leu Thr Val Ser Pro
 675 680 685
 GTG ATT GTG CTG TCA AAA AAG TTA ATT CAA TTT GCT CCA ATT GGA TTA 2170
 Val Ile Val Leu Ser Lys Lys Leu Ile Gln Phe Ala Pro Ile Gly Leu
 690 695 700
 GTG AAC ATG CTT AAC ACT GGT GGT GCC ATT CAG TCC ATG GAG TTT GAC 2218
 Val Asn Met Leu Asn Thr Gly Gly Ala Ile Gln Ser Met Glu Phe Asp
 705 710 715
 AAC CAC ATA GAT GTG GTC AAA ATT GGG GTT AGG GGT TGT GGG GAG ATG 2266
 Asn His Ile Asp Val Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met
 720 725 730 735
 AAG GTG TTT GCA TCA GAG AAA CCA GTT AGT TGC AAA CTA GAT GGG GTA 2314
 Lys Val Phe Ala Ser Glu Lys Pro Val Ser Cys Lys Leu Asp Gly Val
 740 745 750
 GTT GTA AAA TTT GAT TAT GAG GAT AAA ATG CTG AGA GTG CAA GTT CCC 2362
 Val Val Lys Phe Asp Tyr Glu Asp Lys Met Leu Arg Val Gln Val Pro
 755 760 765
 TGG CCT AGT GCT TCA AAA TTG TCA ATG GTT GAG TTT TTA TTT TGA TCCCT 2412
 Trp Pro Ser Ala Ser Lys Leu Ser Met Val Glu Phe Leu Phe Stop
 770 775 780
 GAAGGTGAAT TTGGGATACT ATGATGTTTG ACTCTCTTTT TAAGTAATAA GAGTCATATT 2472
 TTTCTGTTGT AAAAAAAAAA AAAAAA 2498

(1) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Japanese artichoke (*Stachys sieboldii*)
- (F) TISSUE TYPE: leaves

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Asn Gly Ser Asp Leu Glu Arg Glu Thr Gln Ile Val Val Leu Asp
 1 5 10 15
 Lys Ser Asp Asp Arg Pro Tyr Ile Val Leu Leu Pro Leu Ile Glu Gly
 20 25 30
 Gln Phe Arg Ala Ser Leu Gln Pro Gly Val Asp Asp Phe Ile Asp Ile
 35 40 45
 Cys Val Glu Ser Gly Ser Thr Lys Val Asn Glu Ser Ser Phe Arg Ala
 50 55 60
 Ser Leu Tyr Met His Ala Gly Asp Asp Pro Phe Thr Leu Val Lys Asp
 65 70 75 80

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	Ala	Val	Lys	Val	Ala	Arg	His	His	Leu	Gly	Thr	Phe	Arg	Leu	Leu	Glu
					85					90						95
5	Glu	Lys	Thr	Pro	Pro	Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp
				100					105					110		
	Asp	Ala	Phe	Tyr	Leu	Asn	Val	Gln	Pro	His	Gly	Val	Met	Glu	Gly	Val
			115					120					125			
	Gln	Gly	Leu	Val	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp
			130					135				140				
10	Asp	Gly	Trp	Gln	Ser	Ile	Cys	His	Asp	Asn	Asp	Ala	Leu	Thr	Thr	Glu
			145					150				155				160
	Gly	Met	Gly	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Ile
				165						170					175	
	Lys	Phe	Glu	Glu	Asn	Tyr	Lys	Phe	Arg	Glu	Tyr	Glu	Ser	Pro	Asn	Lys
				180					185					190		
15	Thr	Gly	Pro	Gly	Pro	Asn	Thr	Gly	Met	Gly	Ala	Phe	Ile	Arg	Asp	Met
			195					200					205			
	Lys	Asp	Asn	Phe	Lys	Ser	Val	Asp	Tyr	Val	Tyr	Val	Trp	His	Ala	Leu
			210					215					220			
	Cys	Gly	Tyr	Trp	Gly	Gly	Leu	Arg	Pro	Asn	Val	Pro	Gly	Leu	Pro	Glu
			225					230				235				240
20	Ala	Lys	Leu	Ile	Glu	Pro	Lys	Leu	Thr	Pro	Gly	Leu	Lys	Thr	Thr	Met
				245						250						255
	Glu	Asp	Leu	Ala	Val	Asp	Lys	Ile	Val	Asn	Asn	Gly	Val	Gly	Leu	Val
				260					265					270		
	Pro	Pro	Glu	Phe	Val	Glu	Gln	Met	Tyr	Glu	Gly	Leu	His	Ser	His	Leu
			275					280					285			
25	Glu	Ser	Val	Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	Leu
			290					295					300			
	Glu	Met	Leu	Cys	Glu	Asp	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	Ala
			305					310				315				320
	Tyr	Tyr	Lys	Ala	Leu	Ser	Ser	Ser	Val	Asn	Asn	His	Phe	Asn	Gly	Asn
				325						330					335	
30	Gly	Val	Ile	Ala	Gly	Leu	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly
				340					345					350		
	Thr	Glu	Ala	Ile	Thr	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr
				355				360					365			
35	Asp	Pro	Ser	Gly	Asp	Pro	Asn	Gly	Thr	Phe	Trp	Leu	Gln	Gly	Cys	His
				370				375					380			
	Met	Val	His	Cys	Ala	Tyr	Asn	Ser	Ile	Trp	Met	Gly	Asn	Phe	Ile	His
				385				390				395				400
	Pro	Asp	Trp	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His
				405						410					415	
40	Ala	Ala	Ser	Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Ser
				420					425					430		
	Val	Gly	Lys	His	Asn	Phe	Glu	Leu	Leu	Arg	Ser	Leu	Val	Leu	Pro	Asp
				435				440					445			
	Gly	Ser	Ile	Leu	Arg	Cys	Asp	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys
				450				455					460			
45	Leu	Phe	Glu	Asp	Pro	Leu	His	Asn	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp
				465				470				475				480
	Asn	Tyr	Asn	Lys	Phe	Thr	Gly	Val	Val	Gly	Thr	Phe	Asn	Cys	Gln	Gly
				485						490					495	
	Gly	Gly	Trp	Ser	Arg	Glu	Val	Arg	Arg	Asn	Gln	Cys	Ala	Ala	Glu	Tyr
				500					505					510		
50	Ser	His	Ala	Val	Ser	Ser	Ser	Ala	Gly	Pro	Ser	Asp	Ile	Glu	Trp	Lys
				515				520					525			
	Gln	Gly	Thr	Ser	Pro	Ile	Asp	Val	Asp	Gly	Val	Lys	Thr	Phe	Ala	Leu
				530				535					540			

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Tyr Leu Phe His Glu Lys Lys Leu Val Leu Ser Lys Pro Ser Asp Lys
 545 550 555 560
 Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser
 565 570 575
 Pro Val Lys Thr Leu Ala Asn Cys Thr Val Gln
 580 585

(1) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 2..1762
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

G	ACA	AAC	GGG	TCG	GAT	CTT	GAG	CGG	GAA	ACT	CAA	ATA	GTC	GTG	CTC	46
Thr	Asn	Gly	Ser	Asp	Leu	Glu	Arg	Glu	Thr	Gln	Ile	Val	Val	Leu		
1					5					10					15	
GAC	AAG	TCC	GAC	GAC	AGG	CCC	TAC	ATC	GTG	CTG	CTT	CCG	CTC	ATC	GAG	94
Asp	Lys	Ser	Asp	Asp	Arg	Pro	Tyr	Ile	Val	Leu	Leu	Pro	Leu	Ile	Glu	
				20					25					30		
GGG	CAG	TTT	CGG	GCT	TCC	CTT	CAG	CCC	GGT	GTG	GAT	GAT	TTT	ATC	GAT	142
Gly	Gln	Phe	Arg	Ala	Ser	Leu	Gln	Pro	Gly	Val	Asp	Asp	Phe	Ile	Asp	
			35				40						45			
ATT	TGT	GTC	GAA	AGC	GGG	TCA	ACC	AAG	GTC	AAC	GAG	TCC	TCG	TTC	CGT	190
Ile	Cys	Val	Glu	Ser	Gly	Ser	Thr	Lys	Val	Asn	Glu	Ser	Ser	Phe	Arg	
		50				55					60					
GCT	TCG	CTC	TAC	ATG	CAC	GCC	GGT	GAT	GAC	CCT	TTT	ACC	CTG	GTG	AAG	238
Ala	Ser	Leu	Tyr	Met	His	Ala	Gly	Asp	Asp	Pro	Phe	Thr	Leu	Val	Lys	
		65				70				75						
GAC	GCC	GTG	AAG	GTG	GCG	CGC	CAC	CAC	CTC	GGG	ACG	TTC	AGG	CTG	CTG	286
Asp	Ala	Val	Lys	Val	Ala	Arg	His	His	Leu	Gly	Thr	Phe	Arg	Leu	Leu	
		80			85					90				95		
GAG	GAG	AAA	ACT	CCG	CCG	GGG	ATC	GTC	GAC	AAA	TTC	GGG	TGG	TGC	ACG	334
Glu	Glu	Lys	Thr	Pro	Pro	Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	
			100						105					110		
TGG	GAT	GCG	TTC	TAC	CTC	AAC	GTC	CAG	CCC	CAC	GGC	GTT	ATG	GAG	GGC	382
Trp	Asp	Ala	Phe	Tyr	Leu	Asn	Val	Gln	Pro	His	Gly	Val	Met	Glu	Gly	
		115						120					125			
GTG	CAG	GGG	CTG	GTT	GAC	GGC	GGA	TGT	CCG	CCG	GGG	CTG	GTG	TTG	ATC	430
Val	Gln	Gly	Leu	Val	Asp	Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	
		130				135						140				
GAC	GAC	GGG	TGG	CAG	TCC	ATT	TGT	CAC	GAC	AAC	GAC	GCG	CTC	ACC	ACC	478
Asp	Asp	Gly	Trp	Gln	Ser	Ile	Cys	His	Asp	Asn	Asp	Ala	Leu	Thr	Thr	
		145				150				155						
GAG	GGG	ATG	GGG	AGA	ACC	TCC	GCC	GGA	GAG	CAA	ATG	CCC	TGC	AGG	TTG	526
Glu	Gly	Met	Gly	Arg	Thr	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	
		160				165				170					175	

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	ATC	AAG	TTT	GAG	GAG	AAT	TAC	AAG	TTC	AGG	GAG	TAC	GAG	AGC	CCG	AAT	574
	Ile	Lys	Phe	Glu	Glu	Asn	Tyr	Lys	Phe	Arg	Glu	Tyr	Glu	Ser	Pro	Asn	
					180					185						190	
5	AAA	ACT	GGG	CCG	GGC	CCG	AAT	ACG	GGG	ATG	GGG	GCC	TTT	ATT	CGT	GAC	622
	Lys	Thr	Gly	Pro	Gly	Pro	Asn	Thr	Gly	Met	Gly	Ala	Phe	Ile	Arg	Asp	
				195					200						205		
	ATG	AAG	GAC	AAT	TTC	AAG	AGT	GTG	GAC	TAC	GTG	TAC	GTG	TGG	CAT	GCG	670
	Met	Lys	Asp	Asn	Phe	Lys	Ser	Val	Asp	Tyr	Val	Tyr	Val	Trp	His	Ala	
				210				215					220				
10	TTG	TGT	GGT	TAT	TGG	GGC	GGG	CTC	AGG	CCC	AAT	GTT	CCG	GGC	CTG	CCC	718
	Leu	Cys	Gly	Tyr	Trp	Gly	Gly	Leu	Arg	Pro	Asn	Val	Pro	Gly	Leu	Pro	
		225				230						235					
	GAG	GCT	AAG	CTC	ATT	GAG	CCC	AAA	CTG	ACT	CCT	GGG	CTT	AAG	ACC	ACC	766
	Glu	Ala	Lys	Leu	Ile	Glu	Pro	Lys	Leu	Thr	Pro	Gly	Leu	Lys	Thr	Thr	
15		240			245						250				255		
	ATG	GAA	GAT	TTG	GCT	GTT	GAT	AAG	ATT	GTC	AAC	AAT	GGC	GTG	GGT	CTG	814
	Met	Glu	Asp	Leu	Ala	Val	Asp	Lys	Ile	Val	Asn	Asn	Gly	Val	Gly	Leu	
				260					265					270			
	GTC	CCA	CCG	GAG	TTT	GTT	GAA	CAA	ATG	TAT	GAA	GGA	TTA	CAT	TCA	CAT	862
20	Val	Pro	Pro	Glu	Phe	Val	Glu	Gln	Met	Tyr	Glu	Gly	Leu	His	Ser	His	
				275					280				285				
	CTC	GAA	TCT	GTG	GGG	ATT	GAT	GGA	GTC	AAA	GTT	GAC	GTC	ATC	CAT	TTG	910
	Leu	Glu	Ser	Val	Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	
		290					295					300					
	TTG	GAA	ATG	TTG	TGT	GAA	GAC	TAT	GGT	GGG	AGA	GTG	GAC	TTA	GCC	AAG	958
25	Leu	Glu	Met	Leu	Cys	Glu	Asp	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	
		305					310					315					
	GCT	TAT	TAC	AAG	GCC	TTA	TCA	AGC	TCA	GTT	AAC	AAC	CAC	TTC	AAC	GGC	1006
	Ala	Tyr	Tyr	Lys	Ala	Leu	Ser	Ser	Ser	Val	Asn	Asn	His	Phe	Asn	Gly	
		320			325						330				335		
	AAC	GGC	GTC	ATC	GCT	GGC	CTG	GAG	CAC	TGC	AAT	GAC	TTC	ATG	TTT	CTC	1054
30	Asn	Gly	Val	Ile	Ala	Gly	Leu	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	
				340					345					350			
	GGA	ACC	GAG	GCC	ATT	ACC	TTG	GGT	CGT	GTC	GGG	GAT	GAT	TTT	TGG	TGC	1102
	Gly	Thr	Glu	Ala	Ile	Thr	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	
				355					360				365				
35	ACT	GAT	CCA	TCT	GGA	GAT	CCC	AAT	GGC	ACG	TTC	TGG	TTG	CAA	GGG	TGT	1150
	Thr	Asp	Pro	Ser	Gly	Asp	Pro	Asn	Gly	Thr	Phe	Trp	Leu	Gln	Gly	Cys	
			370				375						380				
	CAC	ATG	GTG	CAC	TGC	GCC	TAC	AAC	AGC	ATA	TGG	ATG	GGT	AAT	TTC	ATC	1198
	His	Met	Val	His	Cys	Ala	Tyr	Asn	Ser	Ile	Trp	Met	Gly	Asn	Phe	Ile	
		385				390						395					
40	CAC	CCT	GAT	TGG	GAC	ATG	TTT	CAA	TCG	ACT	CAC	CCT	TGC	GCT	GAA	TTC	1246
	His	Pro	Asp	Trp	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	
		400				405					410				415		
	CAC	GCT	GCC	TCA	CGA	GCC	ATC	TCC	GGC	GGG	CCC	ATT	TAC	GTC	AGT	GAC	1294
	His	Ala	Ala	Ser	Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	
				420					425					430			
45	TCG	GTC	GGA	AAG	CAC	AAC	TTC	GAG	CTC	CTT	AGG	AGC	CTC	GTT	CTT	CCC	1342
	Ser	Val	Gly	Lys	His	Asn	Phe	Glu	Leu	Leu	Arg	Ser	Leu	Val	Leu	Pro	
				435				440					445				
	GAT	GGC	TCC	ATC	CTC	CGT	TGT	GAT	TAC	TAC	GCG	CTT	CCG	ACT	CGC	GAT	1390
	Asp	Gly	Ser	Ile	Leu	Arg	Cys	Asp	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	
50				450			455						460				
	TGC	CTC	TTT	GAA	GAT	CCA	CTT	CAC	AAT	GGC	AAG	ACT	ATG	CTC	AAA	ATT	1438
	Cys	Leu	Phe	Glu	Asp	Pro	Leu	His	Asn	Gly	Lys	Thr	Met	Leu	Lys	Ile	
		465				470						475					

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TGG AAT TAT AAC AAG TTC ACC GGA GTT GTC GGA ACT TTC AAC TGC CAA 1486
 Trp Asn Tyr Asn Lys Phe Thr Gly Val Val Gly Thr Phe Asn Cys Gln
 480 485 490 495
 GGT GGC GGG TGG AGC CGG GAA GTG CGT CGC AAC CAA TGC GCT GCC GAG 1534
 Gly Gly Gly Trp Ser Arg Glu Val Arg Arg Asn Gln Cys Ala Ala Glu
 500 505 510
 TAT TCC CAC GCC GTC TCC TCT AGC GCT GGT CCG AGT GAC ATT GAG TGG 1582
 Tyr Ser His Ala Val Ser Ser Ser Ala Gly Pro Ser Asp Ile Glu Trp
 515 520 525
 AAG CAA GGA ACG AGT CCG ATC GAC GTC GGC GTC AAA ACA TTC GCG 1630
 Lys Gln Gly Thr Ser Pro Ile Asp Val Asp Gly Val Lys Thr Phe Ala
 530 535 540
 TTG TAC CTA TTC CAC GAG AAG AAA CTC GTC CTT TCT AAG CCA TCA GAC 1678
 Leu Tyr Leu Phe His Glu Lys Lys Leu Val Leu Ser Lys Pro Ser Asp
 545 550 555
 AAA ATC GAC ATC ACG CTT GAG CCC TTC GAT TTT GAG CTG ATA ACC GTT 1726
 Lys Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val
 560 565 570 575
 TCT CCA GTC AAA ACT CTA GCC AAT TGC ACC GTC CAA 1762
 Ser Pro Val Lys Thr Leu Ala Asn Cys Thr Val Gln
 580 585

(1) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: corn (Zea mays L.)
- (B) STRAIN: Pioneer 3358
- (F) TISSUE TYPE: leaves

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala Ile
 5 10 15
 Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp Phe
 20 25 30
 Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu Arg Cys
 35 40 45
 Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro Leu
 50 55 60
 His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe Ala
 65 70 75 80
 Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu
 85 90 95
 Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala
 100 105 110
 Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro
 115 120 125
 Gly Val Ser Val Lys Asp Val Ser Gln Phe Ala Val Tyr Ala Val Glu
 130 135 140
 Ala Arg Thr Leu Gln Leu Leu Arg Pro Asp Glu Gly Val Asp Leu Thr
 145 150 155 160

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Leu Gln Pro Phe Thr Tyr Glu Leu Phe Val Val Ala Pro Val Arg Val
 165 170 175
 Ile Ser His Glu Arg Ala Ile Lys Phe Ala Pro Ile Gly Leu Ala Asn
 180 185 190
 Met Leu Asn Thr Ala Gly Ala Val Gln Ala Phe Glu Ala Lys Lys Asp
 195 200 205
 Ala Ser Gly Val Thr Ala Glu Val Phe Val Lys Gly Ala Gly Glu Leu
 210 215 220
 Val Ala Tyr Ser Ser Ala Thr Pro Arg Leu Cys Lys Val Asn Gly Asp
 225 230 235 240
 Glu Ala Glu Phe Thr Tyr Lys Asp Gly Val Val Thr Val Asp Val Pro
 245 250 255
 Trp Ser Gly Ser Ser Ser Lys Leu Cys Cys Val Gln Tyr Val Tyr Stop
 260 265 270

(1) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 2..817
- (C) IDENTIFICATION METHOD: by experiment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

C CAG TCC ACG CAC CCC TGC GCC GCC TTC CAC GCC GCG TCC CGC GCC 46
 Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala
 5 10 15
 ATC TCC GGC GGG CCC ATC TAC GTC AGC GAC TCG GTG GGG CAG CAC GAC 94
 Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp
 20 25 30
 TTC GCG CTG CTC CGC CGC CTG GCG CTC CCC GAC GGC ACC GTC CTC CGG 142
 Phe Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu A
 35 40 45
 TGC GAG GGC CAC GCG CTG CCC ACG CGC GAC TGC CTC TTC GCC GAC CCG 190
 Cys Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro
 50 55 60
 CTC CAC GAC GGC CGG ACC GTG CTC AAG ATC TGG AAC GTG AAC CGC TTC 238
 Leu His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe
 65 70 75
 GCC GGC GTC GTC GGC GCC TTC AAC TGC CAG GGC GGC GGG TGG AGC CCC 286
 Ala Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro
 80 85 90 95
 GAG GCG CGG CGG AAC AAG TGC TTC TCG GAG TTC TCC GTG CCC CTG GCC 334
 Glu Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala
 100 105 110
 GCG CGC GCC TCG CCG TCC GAC GTC GAG TGG AAG AGC GGC AAG GCG GGG 382
 Ala Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly
 115 120 125

	CCA	GGC	GTC	AGC	GTC	AAG	GAC	GTC	TCC	CAG	TTC	GCC	GTG	TAC	GCG	GTC	430
	Pro	Gly	Val	Ser	Val	Lys	Asp	Val	Ser	Gln	Phe	Ala	Val	Tyr	Ala	Val	
			130					135						140			
5	GAG	GCC	AGG	ACG	CTG	CAG	CTG	CGC	CCC	GAC	GAG	GGC	GTC	GAC	CTC		478
	Glu	Ala	Arg	Thr	Leu	Gln	Leu	Leu	Arg	Pro	Asp	Glu	Gly	Val	Asp	Leu	
			145				150					155					
	ACG	CTG	CAG	CCC	TTC	ACC	TAC	GAG	CTC	TTC	GTC	GTT	GCC	CCC	GTG	CGC	526
	Thr	Leu	Gln	Pro	Phe	Thr	Tyr	Glu	Leu	Phe	Val	Val	Ala	Pro	Val	Arg	
	160					165				170						175	
10	GTC	ATC	TCG	CAT	GAG	CGG	GCC	ATC	AAG	TTC	GCG	CCC	ATC	GGA	CTC	GCC	574
	Val	Ile	Ser	His	Glu	Arg	Ala	Ile	Lys	Phe	Ala	Pro	Ile	Gly	Leu	Ala	
				180					185						190		
	AAC	ATG	CTC	AAC	ACC	GCC	GGC	GCC	GTG	CAG	GCG	TTC	GAG	GCC	AAG	AAA	622
	Asn	Met	Leu	Asn	Thr	Ala	Gly	Ala	Val	Gln	Ala	Phe	Glu	Ala	Lys	Lys	
15				195					200				205				
	GAT	GCT	AGC	GGC	GTC	ACG	GCA	GAG	GTG	TTC	GTG	AAG	GGC	GCA	GGG	GAG	670
	Asp	Ala	Ser	Gly	Val	Thr	Ala	Glu	Val	Phe	Val	Lys	Gly	Ala	Gly	Glu	
			210					215					220				
	CTG	GTG	GCG	TAC	TCG	TCG	GCG	ACG	CCC	AGG	CTC	TGC	AAG	GTG	AAC	GGC	718
20	Leu	Val	Ala	Tyr	Ser	Ser	Ala	Thr	Pro	Arg	Leu	Cys	Lys	Val	Asn	Gly	
			225					230				235					
	GAC	GAG	GCC	GAG	TTC	ACG	TAC	AAG	GAC	GGC	GTG	GTC	ACC	GTC	GAC	GTG	766
	Asp	Glu	Ala	Glu	Phe	Thr	Tyr	Lys	Asp	Gly	Val	Val	Thr	Val	Asp	Val	
	240					245				250					255		
	CCG	TGG	TCG	GGG	TCG	TCG	TCG	AAG	CTG	TGT	TGC	GTC	CAG	TAC	GTC	TAC	814
25	Pro	Trp	Ser	Gly	Ser	Ser	Ser	Lys	Leu	Cys	Cys	Val	Gln	Tyr	Val	Tyr	
				260					265						270		
	TGA	GCCG	GACGGG	CCGATG	ACTC	TGCGTCTCTG	CTCCCTGCTG	GCCTGCTCAG	GAC								873
	Stop																
	ATAATCTAAT	GTTTAGAGCT	TACCAGGTTT	TACAGCTCTA	TCAGTTTACT	TTTGTTTTTC											933
30	TGCTCTTCGT	TTTTTAAGAA	TTATTTCTAT	TGTGTGAATT	AATGAGTGCT	TTCCTTCTAA											993
	AAA																996

Claims

1. A nucleic acid molecule encoding a plant raffinose synthetase, said synthetase being capable of producing raffinose by combining a D-galactosyl group through an $\alpha(1\rightarrow6)$ bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule, said nucleic acid molecule being selected from the group consisting of:
 - (a) nucleic acid molecules encoding a protein with the amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, and SEQ ID NO:7;
 - (b) nucleic acid molecules comprising the coding region of the nucleotide sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8;
 - (c) nucleic acid molecules hybridizing to the complementary strand of a nucleic acid molecule indicated under (a) or (b);
 - (d) nucleic acid molecules the sequence of which differs from the sequence of a nucleic acid molecule of any one of (a) to (c) due to the degeneracy of the genetic code; and
 - (e) a fragment of any of the nucleic acid molecules of any one of (a) to (d).
2. The nucleic acid molecule encoding a plant raffinose synthetase according to claim 1, wherein the plant is a dicotyledon, preferably a leguminous plant, preferably a broad bean or soybean, or a lamiaeous plant, preferably a Japanese artichoke, or a monocotyledon, preferably a gramineous plant, preferably corn.
3. A probe or primer that specifically hybridizes to a nucleic acid molecule of claim 1 or 2.

4. The probe or primer of claim 3 that has a length of at least 15, 17, 21 or 50 nucleotides.
5. A chimeric gene comprising the nucleic acid molecule of claim 1 or 2, or the probe or primer of claim 3 or 4.
6. The chimeric gene of claim 5 functionally linked to a promoter.
7. A plasmid comprising a nucleic acid molecule of claim 1 or 2, optionally in functional combination with a promoter, or a chimeric gene of claim 5 or 6.
8. A host organism containing the chimeric gene of claim 5 or 6, or the plasmid of claim 7.
9. The host organism of claim 8 which is a microorganism, a plant cell or a plant.
10. A method for the production of a raffinose synthetase protein or a portion thereof, comprising the steps of isolating and purifying a raffinose synthetase protein or a portion thereof from a culture obtained by cultivating the host organism of claim 8 or 9.
11. A raffinose synthetase protein encoded by the nucleic acid molecule of claim 1 or 2 or obtained by the method of claim 10.
12. An antisense nucleic acid molecule or a ribozyme specifically hybridizing or binding to a nucleic acid molecule of claim 1 or 2.
13. A method for modifying metabolism of a derived host organism, which comprises introducing the nucleic acid molecule, probe, primer or chimeric gene of any one of claims 1 to 6 or an antisense nucleic acid molecule or ribozyme of claim 12 into said host organism or a cell thereof, so that the content of the raffinose family oligosaccharides in said host organism or cell thereof is changed.
14. A raffinose synthetase protein related to the raffinose synthetase protein of claim 11 by deletion, replacement, modification or addition of one or several amino acids.
15. An anti-raffinose synthetase antibody capable of binding to the raffinose synthetase protein of claim 11 or 14.
16. Use of the anti-raffinose synthetase antibody of claim 15 for the detection of a raffinose synthetase protein.
17. A method for the detection of a raffinose synthetase gene or a fragment thereof which comprises hybridizing a probe of claim 3 or 4 to an organism-derived genomic DNA or cDNA fragment, and detecting the presence of hybridization.
18. A method for the amplification of a raffinose synthetase gene or a part thereof, which comprises annealing the primer of claim 3 or 4 to organism-derived genomic DNA or cDNA, and amplifying the resulting DNA fragment.
19. The method of claim 18 wherein the DNA fragment is amplified by polymerase chain reaction (PCR).
20. The method of any one of claims 17 to 19, wherein the organism is a plant.
21. A method for obtaining a raffinose synthetase gene, comprising the steps of identifying a DNA fragment containing a raffinose synthetase gene or a gene fragment thereof by the method of any one of claims 17 to 20, and isolating and purifying the DNA fragment identified.
22. A raffinose synthetase gene obtained by the method of claim 21.

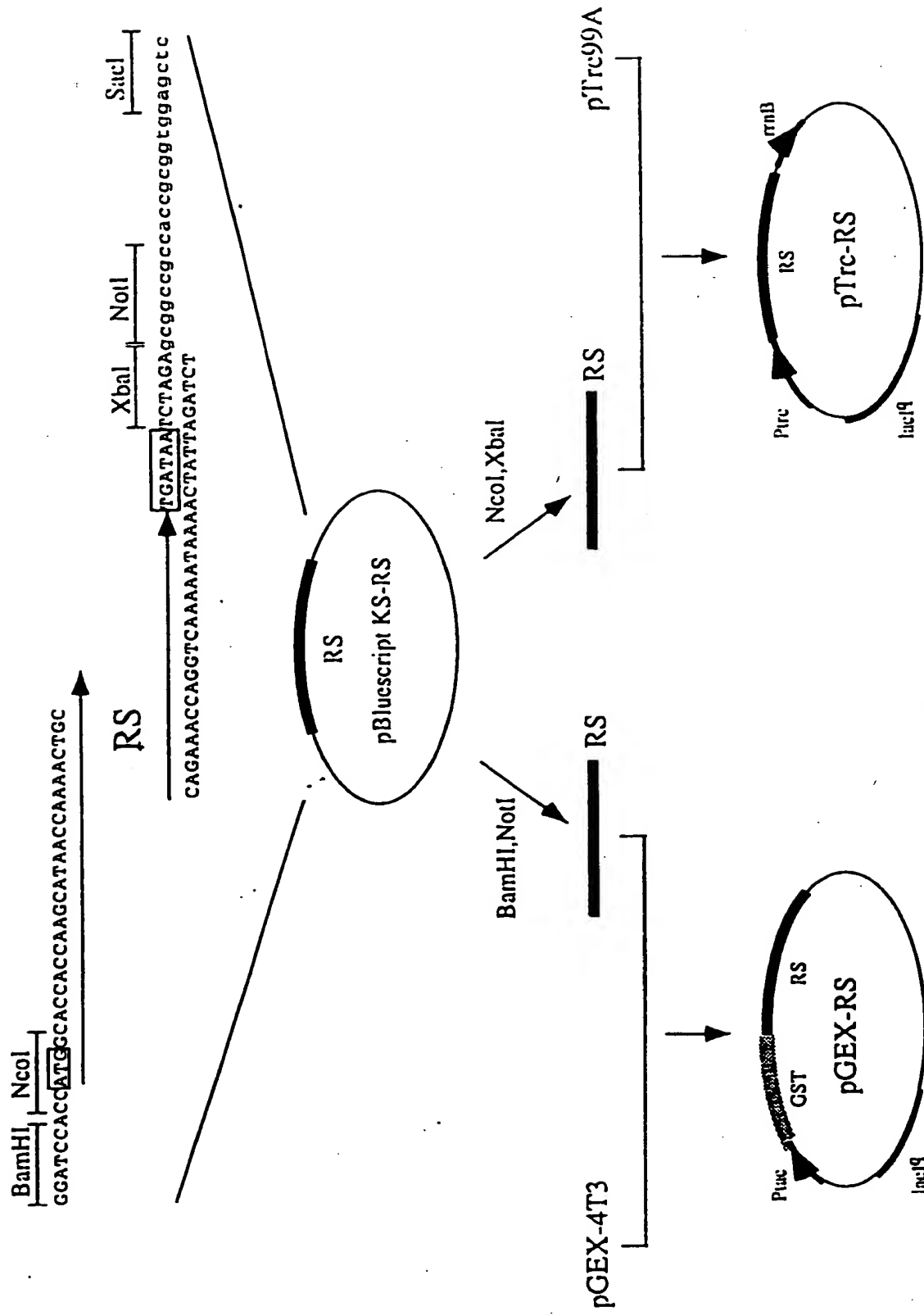


Fig. 1

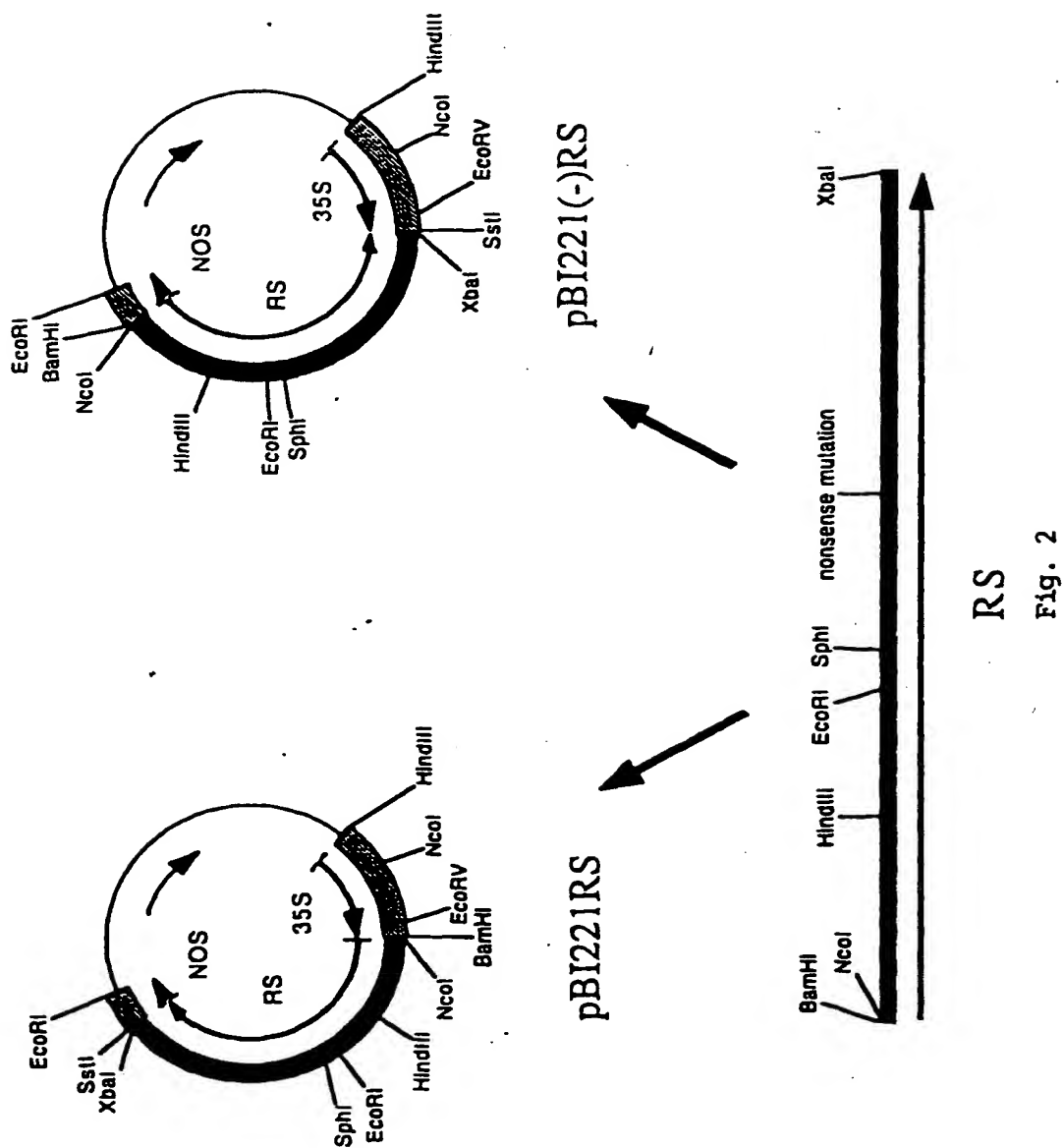


Fig. 2

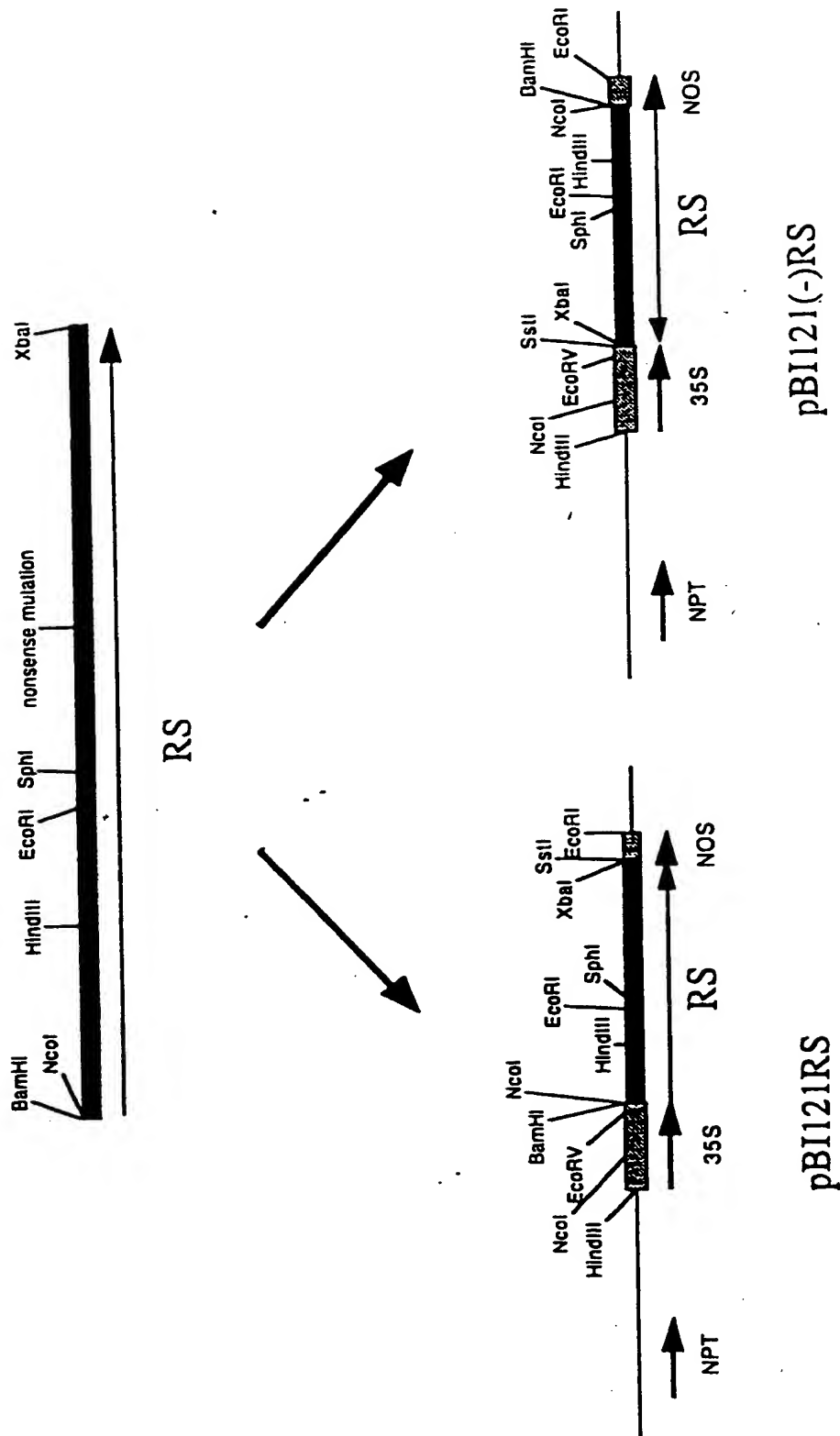


Fig. 3